

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 09:09:19 ; Search time 15 Seconds
(without alignments)
653.189 Million cell updates/sec

Title: US-09-593-288-2

Perfect score: 1731
Sequence: 1 SSKGKKRNPGLIKIPKEAF.....TLHESKGTVDVAFVKLLGD 333

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:**
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:**
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:**
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:**
- 5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:**
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1731	100.0	334	1	US-08-530-950-4
2	1731	100.0	334	3	US-08-576-240-2
3	1731	100.0	334	4	US-08-888-429A-4
4	1731	100.0	334	4	US-09-149-879-4
5	1367	79.0	318	4	US-08-888-429A-2
6	1359	78.5	318	4	US-08-530-950-2
7	1359	78.5	318	4	US-09-149-879-2
8	1358	78.5	318	4	US-08-446-083-2
9	919	53.1	333	4	US-08-888-429A-8
10	919	53.1	333	4	US-08-530-950-10
11	919	53.1	339	2	US-08-874-186-92
12	919	53.1	339	4	US-08-888-429A-10
13	919	53.1	339	4	US-09-149-879-10
14	916.5	52.9	363	1	US-08-530-950-6
15	916.5	52.9	363	4	US-08-888-429A-6
16	916.5	52.9	363	4	US-09-149-879-6
17	906	52.3	393	1	US-08-530-950-8
18	906	52.3	393	4	US-08-888-429A-8
19	833	48.1	185	4	US-09-149-879-8
20	698	40.3	393	4	US-09-384-162-11
21	697	40.3	435	4	US-08-888-429A-21
22	694	40.1	389	4	US-09-446-754-2
23	694	40.1	419	4	US-08-888-429A-20
24	694	40.1	419	4	US-09-446-754-6
25	694	40.1	468	4	US-09-446-754-4
26	690.5	39.9	453	4	US-08-888-429A-32
27	687	39.7	468	4	US-09-446-754-10

28	685	39.6	380	4	US-08-888-429A-30	Sequence 30, Appl
29	683.5	39.5	346	4	US-08-888-429A-18	Sequence 18, Appl
30	609.5	35.2	367	4	US-08-888-429A-13	Sequence 13, Appl
31	606	35.0	668	1	US-08-530-950-13	Sequence 13, Appl
32	606	35.0	668	4	US-09-149-879-13	Sequence 13, Appl
33	600	34.7	405	4	US-08-888-429A-22	Sequence 22, Appl
34	587	33.9	393	1	US-08-423-399B-33	Sequence 33, Appl
35	587	33.9	393	4	US-08-530-950-11	Sequence 11, Appl
36	587	33.9	393	4	US-08-888-429A-11	Sequence 11, Appl
37	587	33.9	393	4	US-09-149-879-11	Sequence 11, Appl
38	583	33.7	400	2	US-08-878-988-17	Sequence 17, Appl
39	583	33.7	400	4	US-09-272-796-17	Sequence 17, Appl
40	579	33.4	267	2	US-07-857-224B-37	Sequence 37, Appl
41	566	32.7	400	4	US-08-530-950-12	Sequence 12, Appl
42	566	32.7	400	4	US-09-149-879-12	Sequence 12, Appl
43	563	32.5	400	4	US-08-888-429A-12	Sequence 12, Appl
44	557	32.2	400	2	US-08-878-988-3	Sequence 3, Appl
45	557	32.2	400	4	US-09-272-796-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-530-950-4
Sequence 4, Application US/08530950
Patent No. 5736381
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Ralgaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: 19-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-530-950-4
Query Match 100.0% Score 1731: DB 1: Length 334:
Best Local Similarity 100.0%: Pred. No. 2.2e-165;
Matches 333: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Publication

Db	2	SQSKGKRNPBLKIPKEAFEQPOTSSTPRDDLSKACISIGNQNEFVKADDEPIMELGR	61
QY	61	GAYGVVERKMRHVPSQOIMAVKRIRATVNSQEQKRLMLDIDSMRYVDCFFTYFVYALGR	120
Db	62	GAYGVVERMRHVPSQOIMAVKRIRATVNSQEQKRLMLDIDSMRYVDCFFTYFVYALGR	121
QY	121	EGDWIMCKELMDTSLDKFYKQYIDGQITPEDIILKIAVSIYKALEHLSKLSVIRHDYK	180
Db	122	EGDWIMCKELMDTSLDKFYKQYIDGQITPEDIILKIANSIYKALEHLSKLSVIRHDYK	181
QY	181	PSNVLINALGOVKMCDFGISGYLVDSVAKTIDAGCKPYAPERINELNOKGYSVSDTW	240
Db	182	PSNVLINALGOVKMCDFGISGYLVDSVAKTIDAGCKPYAPERINELNOKGYSVSDTW	241
QY	241	SLGTMIELATILRFYPDWSGTPFOOLKOVEEPPSPDLPADKFAEEVDFTSQCLKNNKE	300
Db	242	SLGTMIELATILRFYPDWSGTPFOOLKOVEEPPSPDLPADKFAEEVDFTSQCLKNNKE	301
QY	301	RPTYPELMOHPFTLHESKGLDVASFVKILIGD	333
Db	302	RPTYPELMOHPFTLHESKGLDVASFVKILIGD	334

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US-08-576-240-2
: Sequence 2, Application US/08576240
: Patent No. 6074862
: GENERAL INFORMATION:
: APPLICANT: Stein, Bernd
: APPLICANT: Yang, Maria
: TITLE OF INVENTION: MITOGEN-ACTIVATED PROTEIN KINASE
: TITLE OF INVENTION: MEK6 AND METHODS OF USE THEREFOR
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SEED and BERRY LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DO5
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/576,240
: FILING DATE: 20-DEC-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Makl, David J.
: REGISTRATION NUMBER: 31,392
: REFERENCE/DOCKET NUMBER: 860098.403
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4500
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 334 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-576-240-2

Query Match          100.0%; Score 1731; DB 3; Length 334;
Best Local Similarity 100.0%; Pred. No. 2,2e-165;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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2  SOSGSKRNPLKLTIPKEAFEDQPTSTPPRDLDSKACISIGNONFEVKADDELPIMELGR 60

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Qy	61	GAYGVEMKRVHP	SGOIMAVKRIRKRV	TSVSOEKRLLMD	DISMRVDCFFVYFGALFR	120
Qy	62	GAYGVEMKRVHP	SSQIMAVKRIRKRV	TSVSOEKRLLMD	DISMRVDCFFVYFGALFR	121
Db						
Qy	121	EGDVWICMELMD	TSIDKFEYKOVID	KGQITPEDI	LKIAVSYKALEHLSKISV	180
Db	122	EGDVWICMELMD	TSIDKFEYKOVID	KGQITPEDI	LKIAVSYKALEHLSKISV	181
Qy	181	PSNVILNLGOVKMC	DFGISGYLVS	VAKTIDAGCKR	YPAPERINBELNOKGYSV	240
Db	182	PSNVILNLGOVKMC	DFGISGYLVS	VANTIDAGCKR	YPAPERINBELNOKGYSV	241
Qy	241	SLGITMIELALIR	FRPYDSWGT	PPQOLKOV	VEEESPOLDPDKFASEVD	FSOCLKNSKE 300
Db	242	SLGITMIELALIR	FRPYDSWGT	PPQOLKOV	VEEESPOLDPDKFASEVD	FSOCLKNSKE 301
Qy	301	RPTYELMOMHP	FFTLHESKGT	DVASFVKL	ILGD 333	
Db	302	RPTYELMOMHP	FFTLHESKGT	DVASFVKL	ILGD 334	

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1      RESULT 3
2      US-08-888-429A-4
3      ; Sequence 4, Application US/08888429A
4      ; Patent No. 6136596
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: Davis, Roger J.
8      ; APPLICANT: Whitmarsh, Alan
9      ; APPLICANT: Tournier, Cathy
10     ; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
11     ; TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES
12     ; NUMBER OF SEQUENCES: 34
13     ;
14     ; CORRESPONDENCE ADDRESS:
15     ; ADDRESSEE: Fish & Richardson P.C.
16     ; STREET: 225 Franklin Street
17     ; CITY: Boston
18     ; STATE: MA
19     ;
20     ; COUNTRY: USA
21     ; ZIP: 02110-2804
22     ;
23     ; COMPUTER READABLE FORM:
24     ; MEDIUM TYPE: Diskette
25     ; COMPUTER: IBM Compatible
26     ; OPERATING SYSTEM: Windows95
27     ;
28     ; SOFTWARE: FASTSEQ for Windows Version 2.0
29     ;
30     ; CURRENT APPLICATION DATA:
31     ; APPLICATION NUMBER: US/08/888-429A
32     ; FILING DATE: 07-JUL-1997
33     ;
34     ; PRIOR APPLICATION DATA:
35     ; APPLICATION NUMBER: 08/530,950
36     ; FILING DATE: 19-SEP-1995
37     ; APPLICATION NUMBER: 08/446,083
38     ; FILING DATE: 19-MAY-1995
39     ; ATTORNEY/AGENT INFORMATION:
40     ; NAME: Fasse, Peter J.
41     ;
42     ; REGISTRATION NUMBER: 32,983
43     ; REFERENCE/DOCKET NUMBER: 07917/053001
44     ; TELECOMMUNICATION INFORMATION:
45     ; TELEPHONE: 617/542-5070
46     ; TELEFAX: 617/542-8906
47     ;
48     ; TELEX: 299354
49     ;
50     ; INFORMATION FOR SEQ ID NO: 4:
51     ; SEQUENCE CHARACTERISTICS:
52     ; LENGTH: 334 amino acids
53     ; TYPE: amino acid
54     ; TOPOLOGY: linear
55     ; MOLECULE TYPE: protein
56     ; FRAGMENT TYPE: internal
57     ;
58     ; US-08-888-429A-4
59
60     Query Match 100.0%; Score 1731; DB 4; Length 334;
61     Best Local Similarity 100.0%; Pred. No. 2,2e-165;
62     Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY 1 SOSKGRKRNPGIKIKPEAFEPQOTSSPPRDLDSKACISIGNONFEVKADDEPIIMELGR 60
Db 2 SOSKGRKRNPGIKIKPEAFEPQOTSSPPRDLDSKACISIGNONFEVKADDEPIIMELGR 61
QY 61 GAYGVEKRRHVPSSQIMAVKRIATVNSOEKRLMDLDSMRVDCPFTVYFGALFR 120
Db 62 GAYGVEKRRHVPSSQIMAVKRIATVNSOEKRLMDLDSMRVDCPFTVYFGALFR 121
QY 121 EGDVWICMELMDTSLDKFYKQVIDKGQITIPEDILGKIAVSIVKALEHLHSKLSVYHRDVK 180
Db 122 EGDVWICMELMDTSLDKFYKQVIDKGQITIPEDILGKIAVSIVKALEHLHSKLSVYHRDVK 181
QY 181 PSNVILNALGVKMDCFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDIW 240
Db 182 PSNVILNALGVKMDCFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDIW 241
QY 241 SLGITMIELALIRFPYDSWGTFFPQOLKQVVEEPPQLPADKFSAEFVDFTSOCLKKNKSKE 300
Db 242 SLGITMIELALIRFPYDSWGTFFPQOLKQVVEEPPQLPADKFSAEFVDFTSOCLKKNKSKE 301
QY 301 RPTYPELMQHPPFTLHESKGTDVASFVKLLIGD 333
Db 302 RPTYPELMQHPPFTLHESKGTDVASFVKLLIGD 334

RESULT 4

US-09-149-879-4
Sequence 4, Application US/09149879
Patent No. 6174676
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Rainsaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,879
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-149-879-4

Query Match 100.0%; Score 1731; DB 4; Length 334;
Best Local Similarity 100.0%; Pred. No. 2.2e-165;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOSKGRKRNPGIKIKPEAFEPQOTSSPPRDLDSKACISIGNONFEVKADDEPIIMELGR 60
Db 2 SOSKGRKRNPGIKIKPEAFEPQOTSSPPRDLDSKACISIGNONFEVKADDEPIIMELGR 61
QY 61 GAYGVEKRRHVPSSQIMAVKRIATVNSOEKRLMDLDSMRVDCPFTVYFGALFR 120
Db 62 GAYGVEKRRHVPSSQIMAVKRIATVNSOEKRLMDLDSMRVDCPFTVYFGALFR 121
QY 121 EGDVWICMELMDTSLDKFYKQVIDKGQITIPEDILGKIAVSIVKALEHLHSKLSVYHRDVK 180
Db 122 EGDVWICMELMDTSLDKFYKQVIDKGQITIPEDILGKIAVSIVKALEHLHSKLSVYHRDVK 181
QY 181 PSNVILNALGVKMDCFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDIW 240
Db 182 PSNVILNALGVKMDCFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDIW 241
QY 241 SLGITMIELALIRFPYDSWGTFFPQOLKQVVEEPPQLPADKFSAEFVDFTSOCLKKNKSKE 300
Db 242 SLGITMIELALIRFPYDSWGTFFPQOLKQVVEEPPQLPADKFSAEFVDFTSOCLKKNKSKE 301
QY 301 RPTYPELMQHPPFTLHESKGTDVASFVKLLIGD 333
Db 302 RPTYPELMQHPPFTLHESKGTDVASFVKLLIGD 334

RESULT 5

US-08-888-429A-2
Sequence 2, Application US/08888429A
Patent No. 6136596
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Whitmarsh, Alan
APPLICANT: Tournier, Cathy
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,429A
FILING DATE: 07-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE: 19-SEP-1995
APPLICATION NUMBER: 08/446,083
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 299354
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear

Fri Jun 6 15:36:17 2003

us-09-593-288-2.rail

Page 6

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REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 07917/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 299354
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-888-429A-8

Query Match 53.1%; Score 919; DB 4; Length 393;
Best Local Similarity 51.3%; Pred. No. 6,5e-84;
Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6

QY 1 SQSKGKKR-----NPLGIKPK-----AFQPOSTSTPPDLDSKACISIG-NDN 44
Db 29 SSMGKKRAKALKLFANPPFKSTARPTLNPNTGYONPHIERLRTHSIESGRLKISPEQH 88
QY 45 FEVKADDELPIMELGRCAGYGYEKKRHYPSGQIMAVKRIRATVYSEOKRIAMDLSMR 104
Db 89 WDTAEDLKDLDGEIRGAGYGVNKKVHPSSGQIMAVKRIRSYDEKEQQLMDLDDVNR 148
QY 105 TVDCEPTVTFYGALFREDDVWVICMELMDTSLDKFYK--QVIDKGQITPEDILGKIAVSI 161
Db 149 SSDCYITVQFIALFREDDGWCWCMELMSTSFQKFKYVYSVD--DVIEEILGKITLTAT 206
QY 162 VKALEHLHSKLSVHRDVKPSPVNLINALQGVKMCQPGISGYLVDSVAKTIDAGCKRYMAP 221
Db 207 VKALNHLTKENLKIHRDIKPSNILLDRSGNIKLCDGISGLVDSTAKTRDGCRTYMAP 266
QY 222 ERINPELNOKGYSVKSDIMSIGITMTIELALRFPPYSWCTPFEQLKQVYEEPSQLPAD- 280
Db 267 ERIDPSASAGQIDVSDWSLGTLTYELATGRPPYKMNVSFDQLQVYVKGDDPQLSNSE 326
QY 281 --KFSAEVDFDTSCQIKKNSKERPTYPPELMOHPEFLHESKIGDVSFVKLLI 331
Db 327 EREFSPSFINFVNLCLTKDESKRPKYKELIKHPFILLMYERAAVEACVYCKIL 379

RESULT 10
US-08-530-950-10
Sequence 10, Application US/08530950
Patent No. 5736381
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Deltjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: 19-SEP-1995
CLASSIFICATION: 435

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ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

US-08-530-950-10

Query Match 53.1%; Score 919; DB 1; Length 399;
Best Local Similarity 51.3%; Pred. No. 6,6e-84;
Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;

1 SOSGKKR-----NPKLTIPK-----AFEDPOTSSPPRLDLSKACISIG-NQN 44
::|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
35 SSMQKRKALKLNENPFKSTAREFLTNPNPGVONPHERLKTHTSISSGKTKISPCH 94
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
45 FEVARADDEPIRELGRGAAYGVYEKMHPVSGOIMAKRIATAVNSOEQRLLMDDISMR 104
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
95 WDTAEDLKDJGEIRGAGVNKAHKSQTMAVKRRISTYDEKEQLMLDDLVNR 154
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
105 TVDCFTVTYGALFREGDWVICMEIMLMTSLDKFYK--QVIDKGOTIPEDLIGKTAVS 161
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155 SSDCYITGYFALFRFGCWCICMELMSTSFDFKYVSVLD-DVIDEELLGITLAT 212
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
162 VKALEHLKSLVIHRDVPSNVNLALOVMCMCDGISGLTVDSVAKTIADGCKPYMAP 221
||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
213 VVALNHKLKENLKIHRDIKPSNILDRSNGIKLCDGISQLVDSTA KTADACRPYMAP 272
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
222 ERINPELNOKGSVSKSDIVMSLGTITIELAILREPPDYSWGTFPFOOLKVYYEEPSPQLPAD- 280
||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
273 EKDIDSAASGGIDVRDWMSGITLVELATGFPYPKMNVSFDQLNQVXGDPPLSNSE 332
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
281 --KFSAEVDFTSQCCLKNSKERPTTPELMQHFFTLHEKSGKGDVASFWVLIL 331
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
333 EEFSFSEINFVNLCTKDES KRKYKELKHFFILMYEEAAVEACTVC KIL 385
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11
US-08-874-186-92
Sequence 92, Application US/08874186
Patent No. 5989885
GENERAL INFORMATION:
APPLICANT: Teng, David H-F.
APPLICANT: Tavligian, Sean V.
APPLICANT: Petry III, William L.
APPLICANT: Skolnick, Mark H.
TITLE OF INVENTION: SPECIFIC MUTATIONS OF MAP KINASE KINASE
TITLE OF INVENTION: 4 (MKK4) IN HUMAN TUMOR CELL LINES IDENTIFY IT AS A TUMOR
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,186
FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/782,482
 FILING DATE: 10-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Saxe, Stephen A.
 REGISTRATION NUMBER: 38,609
 REFERENCE/DOCKET NUMBER: 24884-121392-01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4848
 TELEFAX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 399 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-874-186-92

Query Match 53.1%; Score 919; DB 2; Length 399;
 Best Local Similarity 51.3%; Pred. No. 6,6e-84;
 Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;

QY 1 SOSGKKR-----NPGIKPKE-----AFEOPTSTPPRLDLSKACISIG-NON 44
 DB 35 SSMGKRRKALKLPANPFKSTARFTLNPNPTGVONPHIERLRTHTSISSGKLIKISPECH 94
 QY 45 FEVKADLEPIELMGAGYGVVEKMRHVPSSGOIMAVKRIRATVNSOEOKRLMDIDISMR 104
 DB 95 WDFEADLDKDLGELIGRGAYGVSNKAVHRPSQIMAVKRIRSTVDEKQKOLMDLDVYMR 154
 QY 105 TVDCPTVTFYFGLFREGDVMICMELMDSIDKFK--QVIDKGQITPEDILGKIAVSI 161
 DB 155 SSDCPYIVQFYGFALFREGDVMICMELMDSIDKFKYKYSVLD--DVIPETILGKITLAT 212
 QY 162 VKALEHLSKLSVTHRDVPSNVLLINALGVKMDPFGISGLYVDSVATIDAGCRPYMAP 221
 DB 213 VKALNHLKENLKIITHRDIPSNTLDRSGNKLCDPFGISGLVDSIATKTRDAGCRPYMAP 272
 QY 222 ERINPELNQKGSVKSIDMSLGTMTIELALRFPYDSWGTPEOOLKQVVEEPPOLPAD- 280
 DB 273 ERIDPSASRQGYDVRDWSLGTILYELATGRFPYKMNVSFDDLTQVVKGDPOLDSNSE 332
 QY 281 --KFSAEVDFTSQCCKKNSKERPTYPELMOHPFTLHESKGTDVASFYKLL 331
 DB 333 EREFSPSFTNFVNLCTKDESKRPYKELKHPIILMYERAVEVACVCKIL 385

RESULT 12

US-08-888-429A-10
 Sequence 10, Application US/08888429A
 Patent No. 6136396
 GENERAL INFORMATION:
 APPLICANT: Davis, Roger J.
 APPLICANT: Whitmarsh, Alan
 APPLICANT: Tourner, Cathy
 TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
 TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/888,429A

FILING DATE: 07-JUL-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/530,950
 FILING DATE: 19-SEP-1995
 APPLICATION NUMBER: 08/446,083
 FILING DATE: 19-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Fasse, Peter J.
 REGISTRATION NUMBER: 32,983
 REFERENCE/DOCKET NUMBER: 07917/053001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELETYPE: 299354
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 399 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: Internal
 US-08-888-429A-10

Query Match 53.1%; Score 919; DB 4; Length 399;
 Best Local Similarity 51.3%; Pred. No. 6,6e-84;
 Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;

QY 1 SOSGKKR-----NPGIKPKE-----AFEOPTSTPPRLDLSKACISIG-NON 44
 DB 35 SSMGKRRKALKLPANPFKSTARFTLNPNPTGVONPHIERLRTHTSISSGKLIKISPECH 94
 QY 45 FEVKADLEPIELMGAGYGVVEKMRHVPSSGOIMAVKRIRATVNSOEOKRLMDIDISMR 104
 DB 95 WDFEADLDKDLGELIGRGAYGVSNKAVHRPSQIMAVKRIRSTVDEKQKOLMDLDVYMR 154
 QY 105 TVDCPTVTFYFGLFREGDVMICMELMDSIDKFK--QVIDKGQITPEDILGKIAVSI 161
 DB 155 SSDCPYIVQFYGFALFREGDVMICMELMDSIDKFKYKYSVLD--DVIPETILGKITLAT 212
 QY 162 VKALEHLSKLSVTHRDVPSNVLLINALGVKMDPFGISGLYVDSVATIDAGCRPYMAP 221
 DB 213 VKALNHLKENLKIITHRDIPSNTLDRSGNKLCDPFGISGLVDSIATKTRDAGCRPYMAP 272
 QY 222 ERINPELNQKGSVKSIDMSLGTMTIELALRFPYDSWGTPEOOLKQVVEEPPOLPAD- 280
 DB 273 ERIDPSASRQGYDVRDWSLGTILYELATGRFPYKMNVSFDDLTQVVKGDPOLDSNSE 332
 QY 281 --KFSAEVDFTSQCCKKNSKERPTYPELMOHPFTLHESKGTDVASFYKLL 331
 DB 333 EREFSPSFTNFVNLCTKDESKRPYKELKHPIILMYERAVEVACVCKIL 385

RESULT 13

US-09-149-879-10
 Sequence 10, Application US/09149879
 Patent No. 6174676
 GENERAL INFORMATION:
 APPLICANT: Davis, Roger J.
 APPLICANT: Raugeaud, Joel
 APPLICANT: Gupta, Shashi
 APPLICANT: Derjard, Benoit
 TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
 TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,879
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-149-879-10

Query Match
Best Local Similarity 53.1%; Score 919; DB 4; Length 399;
Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;

QY 1 SOSKGRK-----NPKLIPKE-----AFEPQISSPPRDLDSKACISIG-NON 44
DB 35 SSMQGRKRLKLNFAHPPEKSTAFRLNPNPTGVONPHIRLTHRTSHLESSGKLKISPEOH 94
QY 45 FEVKADDDLEPIMELGAGVAYVEKMRHVPSGOIMAYKRIRATVNSOEKRLMDLDSMR 104
DB 95 WQFTADLKLDELIGAGVAYVKNMVKHPSGOIMAYKRIRATVNSOEKRLMDLDSMR 154
QY 105 TVDCPTVTYFGLFREGDVMICMELMDTSLDFYK---OVIDKGQITPDLIGKIVSI 161
DB 155 SDCPYIYQYFGLFREGDVMICMELMDTSLDFYK---OVIDKGQITPDLIGKIVSI 212
QY 162 VALLEHLKSLVYHNDVPSNVLINALGVKMCDCISGYLVDSVAKTIDAGCPYMAP 221
DB 213 VALNLKLENLKIHRDIKPSNILLDRSGNIKLCDFGISQLVDSIAKTIDAGCPYMAP 272
QY 222 ERINPELNQKGVSKSDISLGTMTLALIRPPYSWGTFFQOLKQVVEEPPSLPAD- 280
DB 273 ERIDPSASRGYDVRSDVMSLGTITLVELATGRFPYPMKNSVDFQDLTVAGDPQLNSE 332
QY 281 --KFSAEFYDFTSQCLKNSKERPTYPELMOHPFTLHESKGTIVASFVKLIL 331
DB 333 EREFSPSFINFVNLCLTKDESKRPKYKELKHPIIMYERAVEVACVCKIL 385

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RESULT 14
US-08-530-950-6
Sequence 6, Application US/08530950
Patent No. 5736381

GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Raingaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Dejard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston

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STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: 19-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-530-950-6

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Query Match
Best Local Similarity 52.9%; Score 916.5; DB 1; Length 363;
Matches 175; Conservative 53; Mismatches 82; Indels 9; Gaps 4;

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QY 20 EOPQTSSTPPRDLDSKACISIG-NONEVKADDEPIMELGAGVAYVEKMRHVPSGOIM 78
DB 33 QNPHIERLRTHSIESSGKLKISPEOHWFADLDELIGIGAGVAYVKNMVKHPSGOIM 92
QY 79 AVKRIRATVNSOEKRLMDLDSMRATVNSOEKRLMDLDSMRATVNSOEKRLMDLDSMR 138
DB 93 AVKRIRATVNSOEKRLMDLDSMRATVNSOEKRLMDLDSMRATVNSOEKRLMDLDSMR 152
QY 139 YK---OVIDKGQITPDLIGKIVSIKSLVYHNDVPSNVLINALGVKMCDCISGYLV 195
DB 153 YK---OVIDKGQITPDLIGKIVSIKSLVYHNDVPSNVLINALGVKMCDCISGYLV 210
QY 196 DFGISGYLVDSVAKTIDAGCPYMAPERINPELNQKGVSKSDISLGTMTLALIRP 255
DB 211 DFGISGYLVDSVAKTIDAGCPYMAPERINPELNQKGVSKSDISLGTMTLALIRP 270
QY 256 YDSWGTFFQOLKQVVEEPPSLPAD---KFSAEFYDFTSQCLKNSKERPTYPELMOHP 312
DB 271 YPKNSVDFQDLTVAGDPQLNSEERFSPFINFVNLCLTKDESKRPKYKELKHPI 330
QY 313 FTLHESKGTIVASFVKLIL 331
DB 331 ILMYERAVEVACVCKIL 349

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RESULT 15
US-08-888-429A-6
Sequence 6, Application US/08888429A
Patent No. 6136596

GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Whitmarsh, Alan
APPLICANT: Tounier, Cathy
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE KINASES
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA

COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,429A
FILING DATE: 07-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE: 19-SEP-1995
APPLICATION NUMBER: 08/446,083
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 299354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-888-429A-6

Query Match 52.9%; Score 916.5; DB 4; Length 363;
Best Local Similarity 54.9%; Pred. No. 1e-83;
Matches 175; Conservative 53; Mismatches 82; Indels 9; Gaps 4;

QY 20 EQPQSTPPRDLSKACISIG-NONEVYKADDEPIMELGRGAGVVEKMRHVPSGQIM 78
DB 33 QNPHIERLRTHSISSGKLIKISPOHMDFTADLKDGLGIGAGVSVNKMVHKPPSGQIM 92
QY 79 AVKRIRATVNSOEQRRLMDDISMRVDCPFTVTFYGLAFREGDVMICMELMDTSLDKF 138
DB 93 AVKRIRSTVDEKEKQKQLMDLDVYMRSSDCPTIYVFGALFREGDCWICMELMSTISFDKF 152
QY 139 YK--QVIDKGQITPEDILKRIAVSVKALEHLHLSKISVIHRDVKPSNVLINALGVKKMC 195
DB 153 YKVVYSYLD--DVIPETILGKITLATVAKALNHLKENLKIIRHDIKPSNILLDRSGNIKLC 210
QY 196 DEGISGYVDSVAKTIDAGCPYMAPERINPELNOKGYSVKSDIWSLGITMIELATLRPP 255
DB 211 DEGISQQLVDSIAKTRDAGCRPYMAPERIDPSASROGYDRSDVWSLGITLYELATGRFP 270
QY 256 YDSMGTPFOOLKQVVEEPPQLPAD--KFSAEFVDFTSQCLKNSKERPTPELMQHPF 312
DB 271 YPKMNSVFDQLIQVVKDPPQLSNSEREERFSPFINFVNLCLTKDESKRPKYKELLKHPF 330
QY 313 FTIHESKGTDVASFVKLIL 331
DB 331 ILMYERAVEVACYVCKIL 349

Search completed: June 6, 2003, 09:12:12
Job time: 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 09:11:34 ; Search time 48 Seconds
(without alignments)
716.229 Million cell updates/sec

Title: US-09-593-288-2

Perfect score: 1731
Sequence: 1 SOSKGRKRNPKIKPEKFAE.....TLHESKGTDVASFVKLILGD 333

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1731	100.0	334	10	US-09-761-569-4
2	1367	79.0	318	9	US-09-981-357A-70
3	1367	79.0	318	9	US-10-059-585-36
4	1359	78.5	318	10	US-09-761-569-2
5	919	53.1	399	10	US-09-761-569-10
6	916.5	52.9	363	10	US-09-761-569-6
7	906	52.3	393	10	US-09-761-569-8
8	606	35.0	668	9	US-10-081-119-20
9	606	35.0	668	10	US-09-761-569-13
10	606	35.0	668	10	US-09-801-368-238
11	587	33.9	389	10	US-09-755-665-36
12	587	33.9	393	9	US-09-918-873-4
13	587	33.9	393	10	US-09-761-569-11
14	566	32.7	400	10	US-09-761-569-12
15	563	32.5	395	10	US-09-755-665-34
16	544	31.4	364	10	US-09-755-665-64
17	531	30.7	392	10	US-09-755-665-35
18	531	30.7	394	10	US-09-755-665-33
19	526	30.4	380	10	US-09-755-665-8

20	502	29.0	363	10	US-09-755-665-63	Sequence 63, Appl
21	502	29.0	369	10	US-09-755-665-16	Sequence 16, Appl
22	481	27.8	515	10	US-09-801-368-384	Sequence 384, App
23	476.5	27.5	508	10	US-09-801-368-212	Sequence 212, App
24	471	27.2	346	10	US-09-828-313-36	Sequence 36, App
25	471	27.2	346	10	US-09-828-313-37	Sequence 37, Appl
26	448.5	25.9	506	10	US-09-801-368-214	Sequence 214, App
27	419	24.2	487	10	US-09-810-808-8	Sequence 8, Appl
28	381	22.0	228	10	US-09-755-665-38	Sequence 38, Appl
29	375	21.7	1360	10	US-09-871-916-2	Sequence 2, Appl
30	370.5	21.4	1239	9	US-09-291-417-13	Sequence 13, Appl
31	368.5	21.3	912	9	US-09-291-417-26	Sequence 26, Appl
32	368.5	21.3	968	9	US-09-291-417-107	Sequence 107, App
33	364.5	21.1	911	9	US-09-291-417-92	Sequence 92, Appl
34	361	20.9	224	10	US-09-755-665-37	Sequence 37, Appl
35	354	20.5	1244	9	US-09-789-390-13	Sequence 13, Appl
36	354	20.5	1273	9	US-09-789-390-11	Sequence 11, Appl
37	354	20.5	1295	9	US-09-789-390-30	Sequence 30, Appl
38	354	20.5	1295	9	US-09-789-390-32	Sequence 32, Appl
39	354	20.5	1295	9	US-09-789-390-34	Sequence 34, Appl
40	354	20.5	1295	9	US-09-789-390-39	Sequence 39, Appl
41	354	20.5	1295	9	US-09-789-390-39	Sequence 9, Appl
42	354	20.5	1303	9	US-09-789-390-35	Sequence 35, Appl
43	354	20.5	1303	9	US-09-789-390-38	Sequence 38, Appl
44	354	20.5	1303	9	US-09-789-390-38	Sequence 38, Appl
45	354	20.5	1312	9	US-10-029-115-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-761-569-4
Sequence 4, Application US/09761569
Patent No. US20020102691A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
Ratigaude, Joel
Gupta, Shashi
Derjard, Benoît
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/761,569
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/057,009
FILING DATE: 1998-04-07
ATTORNEY/AGENT INFORMATION:
NAME: Passee, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 334 amino acids
 TYPE: amino acid
 STRANDEDNESS: No. US20020102691A1 Relevant
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-761-569-4

Query Match 100.0%; Score 1731; DB 10; Length 334;
 Best Local Similarity 100.0%; Pred. No. 2e-146;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOSGKKRNPGLKIPKEAFEPQSTSPRRDLDSKACISIGNONEVKKADLEPIEIGR 60
 DB 2 SOSGKKRNPGLKIPKEAFEPQSTSPRRDLDSKACISIGNONEVKKADLEPIEIGR 61
 QY 61 GAYGVEMKRRVPSQIMAVKRIKATVNSQEQKRLMDIDISMRTVDCPTVFYGFALR 120
 DB 62 GAYGVEMKRRVPSQIMAVKRIKATVNSQEQKRLMDIDISMRTVDCPTVFYGFALR 121
 QY 121 EGDWICMELMDTSLDKFYKQYIDKQGITPEDILGKIAVSIVKALEHLSKLSVIRDYK 180
 DB 122 EGDWICMELMDTSLDKFYKQYIDKQGITPEDILGKIAVSIVKALEHLSKLSVIRDYK 181
 QY 181 PSNVILNALGVKMCDFGIGSYLVDSVAKTIDAGCKPYWAPERINELNOKGYSKSDIM 240
 DB 182 PSNVILNALGVKMCDFGIGSYLVDSVAKTIDAGCKPYWAPERINELNOKGYSKSDIM 241
 QY 241 SLGITMELALIRFPYDSMGPRFPOOLKOVEEPPQLPADKFSAEFVFTSOCLKKNRSE 300
 DB 242 SLGITMELALIRFPYDSMGPRFPOOLKOVEEPPQLPADKFSAEFVFTSOCLKKNRSE 301
 QY 301 RPTYPELMQHPFTLHESKGTVDASFKLILGD 333
 DB 302 RPTYPELMQHPFTLHESKGTVDASFKLILGD 334

RESULT 2
 US-09-981-397A-20
 ; Sequence 20, Application US/09981397A
 ; Publication No. US20030082519A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Axixma Pharmaceuticals AG
 ; APPLICANT: Schubart, Daniel
 ; APPLICANT: Habenberger, Peter
 ; APPLICANT: Stein-Gerlach, Matthias
 ; APPLICANT: Bevec, Dorian
 ; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
 ; FILE REFERENCE: AXM-004.1 US
 ; CURRENT FILING DATE: 2002-06-28
 ; PRIOR APPLICATION NUMBER: 60/240,750
 ; PRIOR FILING DATE: 2000-10-16
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 20
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-981-397A-20

Query Match 79.0%; Score 1367; DB 9; Length 318;
 Best Local Similarity 82.7%; Pred. No. 5.4e-114;
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;

QY 22 POTSSTPRDLDSKACISIGNONEVKKADLEPIEIMELGKAYGVEMKRRVPSQIMAVK 81
 DB 5 PAPTPTPRNDLSRFTITIGDRNFEVADDLVITISLGRGAYGVEMKRRVPSQIMAVK 64
 QY 82 RIRATVNSQEQKRLMDIDISMRTVDCPTVFYGFALFREGDVWICMELMDTSLDKFYK 141
 DB 65 RIRATVNSQEQKRLMDIDISMRTVDCPTVFYGFALFREGDVWICMELMDTSLDKFYK 124

QY 142 VIDKGTIPEDILGKIAVSIVKALEHLSKLSVIRDYKPSNVILNALGVKMCDFGIGS 201
 DB 125 VIDKMTIPEDILGKIAVSIVKALEHLSKLSVIRDYKPSNVILNALGVKMCDFGIGS 184
 QY 202 YLVDVAKTIDAGCKPYWAPERINELNOKGYSKSDIMSGITMELALIRFPYDSMG 261
 DB 185 YLVDVAKTIDAGCKPYWAPERINELNOKGYSKSDIMSGITMELALIRFPYDSMG 244
 QY 262 PFOOLKOVEEPPQLPADKFSAEFVFTSOCLKKNRSEKRPTELMQHPFTLHESKGT 321
 DB 245 PFOOLKOVEEPPQLPADKFSAEFVFTSOCLKKNRSEKRPTELMQHPFTLHESKGT 304
 QY 322 DVASFVKLILGD 333
 DB 305 DIAAFVKILGE 316

RESULT 3
 US-10-059-585-36
 ; Sequence 36, Application US/10059585
 ; Publication No. US20030082776A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ota, Toshio
 ; APPLICANT: Isogai, Takao
 ; APPLICANT: Nishikawa, Tetsuo
 ; APPLICANT: Hayashi, Koji
 ; APPLICANT: Otsuka, Kaori
 ; APPLICANT: Yamamoto, Jun-ichi
 ; APPLICANT: Ishii, Shizuko
 ; APPLICANT: Sugiyama, Tomoyasu
 ; APPLICANT: Wakamatsu, Ai
 ; APPLICANT: Nagai, Keiichi
 ; APPLICANT: Otsuki, Tetsuji
 ; APPLICANT: Funahashi, Shin-ichi
 ; APPLICANT: Senoo, Chiaki
 ; APPLICANT: Nezu, Jun-ichi
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
 ; FILE REFERENCE: 06501-098001
 ; CURRENT FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/05060
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/183,322
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: US 60/159,590
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: JP 2000-118776
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: JP 2000-183767
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: JP 11-248036
 ; PRIOR FILING DATE: 1999-07-29
 ; SOFTWARE: FastSeq for Windows version 4.0
 ; SEQ ID NO: 36
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-059-585-36

Query Match 79.0%; Score 1367; DB 9; Length 318;
 Best Local Similarity 82.7%; Pred. No. 5.4e-114;
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;

QY 22 POTSSTPRDLDSKACISIGNONEVKKADLEPIEIMELGKAYGVEMKRRVPSQIMAVK 81
 DB 5 PAPTPTPRNDLSRFTITIGDRNFEVADDLVITISLGRGAYGVEMKRRVPSQIMAVK 64
 QY 82 RIRATVNSQEQKRLMDIDISMRTVDCPTVFYGFALFREGDVWICMELMDTSLDKFYK 141
 DB 65 RIRATVNSQEQKRLMDIDISMRTVDCPTVFYGFALFREGDVWICMELMDTSLDKFYK 124

10

Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;

QY 1 SOSGKKR-----NGKLTPE-----AFEOQTSPTPRDSDSKACISIG-NQN 44
 Db 35 SSMGGRKALKLNFPNPFKSTARFTLNPNFTGVONPIERLRTHTSSESSKLTSPQCH 94
 QY 45 FEVKADLDLEIMELRGAVGVYVEKRRHVPSSGOIMAVRIRATVNSOERLLMDLDSMR 104
 Db 95 WDTTAEEDLDLGEIGRAVGSYNKMKVPSQIMAVRIRSTVEKEKQKLLMDLDVYMR 154
 QY 105 TVDOPFTVTEYGALFREGDVWICMELMDTSLDKFYK--QYIDKGQITPEDILGKIVSI 161
 Db 155 SSDOPYIVQFYGALFREDDCWCIMELMSTSPDKFYKYVSVLD--DVIPETILGKITAT 212
 QY 162 VKALEHLSKLVTHRDVPSNNVLINLGOVKMDFGISGLYVDSVATIPAGCRPYMAP 221
 Db 213 VKALNHLKENKTIHRDTPSNLLDNRSGNKLCDFGISGLVDSIATRDAGCRPYMAP 272
 QY 222 ERINPELNOKGYSVKSDIWSIGITMIELAILRFPPYDSWGTPEQOLKQVEEPSQLPAD- 280
 Db 273 ERIDPSASRGQYDVRSDVMSIGITLYELATGFRFPKMNVSVDQLQYVVKGDPQLSNSE 332
 QY 281 --KFSAEFVDTSOCLKNKSKERPYPPELMQHPFTLHESKGTDVASFVKLL 331
 Db 333 ERFSPSPINFNILCTFKDESKRPKYKELKHPIITMYEERAVEVACVCKIL 385

RESULT 6
 US-09-761-569-6
 ; Sequence 6, Application US/09761569
 ; Patent No. US20020102691A1

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.
 Ringeaud, Joel
 Gupta, Shashi
 Derijard, Benoît
 TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
 ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
 KINASES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/761,569

FILING DATE: 16-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/057,009

FILING DATE: 1998-04-07

ATTORNEY/AGENT INFORMATION:

NAME: Fasse, J. Peter

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 07917/010001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 363 amino acids

TYPE: amino acid

STRANDEDNESS: No. US20020102691A1 Relevant

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-761-569-6

Query Match

Best Local Similarity 54.9%; Score 916.5; DB 10; Length 363;

Matches 175; Conservative 53; Mismatches 82; Indels 9; Gaps 4;

QY 20 EOPQTSPTPRDSDSKACISIG-NQNFVKADLDLEIMELRGAVGVYVEKRRHVPSSGOIM 78
 Db 33 ONPHIERLRTHTSSESSGKLTISPEQHWDTAEEDLDLGEIGRAVGSYNKMKVPSQIM 92
 QY 79 AVKRIRATVNSOERLLMDLDSMRVDCPTVTEYGALFREGDVWICMELMDTSLDKF 138
 Db 93 AVKRIRSTYDEKQKQLMDLDVYMRSSDOPYIVQFYGALFREDDCWCIMELMSTSPDK 152
 QY 139 YK--QYIDKGQITPEDILGKIVSIKALEHLSKLVTHRDVPSNNVLINLGOVKMC 195
 Db 153 YKYVSVLD--DVIPETILGKITATYKALNHLKENKTIHRDTPSNLLDNRSGNKLCD 210
 QY 196 DFGISGLVDSVAKTIDAGCRPYMAPERINPELNOKGYSVKSDIWSIGITMIELAILRF 255
 Db 211 DFGISGLVDSIAKTRDAGCRPYMAPERIDPSASRGQYDVRSDVMSIGITLYELATGRF 270
 QY 256 YDSWGTPEQOLKQVEEPSQLPAD--KFSAEFVDTSOCLKNKSKERPYPPELMQHPF 312
 Db 271 YPKMNSVFDQLQYVVKGDPQLSNSEERFSPSPINFNILCTFKDESKRPKYKELKHPI 330
 QY 313 FTLHESKGTDVASFVKLL 331
 Db 331 ILMYEERAVEVACVCKIL 349

RESULT 7
 US-09-761-569-8
 ; Sequence 8, Application US/09761569
 ; Patent No. US20020102691A1

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.
 Ringeaud, Joel
 Gupta, Shashi
 Derijard, Benoît

TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
 ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
 KINASES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/761,569

FILING DATE: 16-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/057,009

FILING DATE: 1998-04-07

ATTORNEY/AGENT INFORMATION:

NAME: Fasse, J. Peter

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 07917/010001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
 LENGTH: 393 amino acids
 TYPE: amino acid
 STRANDEDNESS: No. US20020102691A1 Relevant
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-761-569-8

Query Match 52.3%; Score 906; DB 10; Length 393;
 Best Local Similarity 51.0%; Pred. No. 9.4e-73;
 Matches 180; Conservative 56; Mismatches 93; Indels 24; Gaps 6;

QY 1 SSGKGRK-----NPGKIKPK-----AEQOPVTSPPRDLDSKACISIG-NON 44
 DB 29 SSMQGRKALKLNPNPPEKSTARFTLNPNTGVNPHIERLRTHSISSGKLKISPEQH 88
 QY 45 FEVKADDEPIMELGRAGVVEKMRHVPSCQIMAVKRIRATVNSOEQRLLMDLDSMR 104
 DB 89 WDETAEDLKDGLGEIGRAGVSVNKMVHPSQIMAVKRIRSTVDEKEQRLMDLDDVNR 148
 QY 105 TVDCPTVTFYCALFRGDVWICMELMDTSLDKFK---QVIDKQOTIPEDILKIAVSI 161
 DB 149 SSGCPVTVTFYCALFRGDVWICMELMDTSLDKFK---QVIDKQOTIPEDILKIAVSI 206
 QY 162 VVALEHLHSLKSVIHRDVPKSNVNLINALQYKMGDFGSGYLVDSVAKTIDAGCKPYMAP 221
 DB 207 VKALMLHKLKILHRDIKPSNILLDRSGMKIKLDFGSGQLVDSIAKTROGCRPYMAP 266
 QY 222 ERLNPELNQKGYSVKSDISLGTIMELAILRPYDSKGTTPPOOLKOVEEPPOLPAD- 280
 DB 267 ERLDSFASRQGYVSRDVSLSIGTLYELATGRFPYKPNNSVFDQLQYVKGDPQLSNSE 326
 QY 281 --KFSAEVDFETSOCLKNSKREPTPELMQHPFTLHESGTDVASFYKLL 331
 DB 327 EHEFSPTFNFWLCLTKDKSKRKYKELLKHPITLMEERAVEACTYCKTL 379

RESULT 8
 US-10-081-119-20
 ; Sequence 20, Application US/10081119
 ; Publication No. US20030045491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reinhard, Christoph
 ; APPLICANT: Jefferson, Anne B.
 ; APPLICANT: Chan, Vivian W.
 ; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
 ; FILE REFERENCE: 16932.002
 ; CURRENT APPLICATION NUMBER: US/10/081.119
 ; CURRENT FILING DATE: 2002-02-21
 ; PRIOR APPLICATION NUMBER: 60/289,813
 ; PRIOR FILING DATE: 2001-02-21
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 668
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-10-081-119-20

Query Match 35.0%; Score 606; DB 9; Length 668;
 Best Local Similarity 37.3%; Pred. No. 1.1e-45;
 Matches 141; Conservative 73; Mismatches 105; Indels 59; Gaps 12;

QY 4 GKGRNPGLKI-----PKAEQF-QTSSTPRDLDSK----- 35
 DB 265 EGRKRNPGSLINGVOSTSTSSSTEGPHDYGTTPRGNSSNNSGSGGGGLPANFSKY 324
 QY 36 ACISIGNONF-----EVKADDEPIMELGRAGVVEKMRHVPSCQ 76
 DB 325 VDIKSGSLNFAKGLSLSKGIDFNSGSSRITLDELEFDELGNAGNVSQVLAHKPTNV 384
 QY 77 IMAVKIRATVNSOEQRLLMDLDSMRVYDCPTVTFYCALFRGDVWICMELMD-TSL 135

DB 365 IMATKEVRLDEAKFRQITMELEV-LHKNSPYIYDFYAGAFLEGAVYKCMEMYDGSL 443
 QY 136 DFEYKVIDKGTIPEDILKIAVSIYKALEHLSKLSVIRDVKPSNVILNA-LGVYKM 194
 DB 444 KDIYDESEELG-GIDEPOLAFTANAVIHGKELKEQONITHRDVKPNILCSANQGYKL 502
 QY 195 CDFGSGYLVDSVAKTIDAGCKPYMAPERI--NPELNQKGYSVKSDISLGTIMELAI 251
 DB 503 CDFGSGYLVDSVAKTIDAGCKPYMAPERI--NPELNQKGYSVKSDISLGTIMELAI 559
 QY 252 LRFPPY--DSWGPPOOLKQVVEPSPQLADKRSAEVDFETSOCLKNSKREPTPELMQ 309
 DB 560 GRYPPEPTIDNIFSLATVDGPPPLPSDKFSQADQFVSLCLQKIPERRPYALTE 619
 QY 310 HPFTLHESKGTVASFV 327
 DB 620 HPWLKYRNQDVHMEYI 637

RESULT 9
 US-09-761-569-13
 ; Sequence 13, Application US/09761569
 ; Patent No. US20020102691A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Roger J.
 ; Raugeaud, Joel
 ; Gupta, Shashi
 ; Derijard, Benoit
 ; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
 ; ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
 ; KINASES
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/761,569
 ; FILING DATE: 16-Jan-2001
 ; CLASSIFICATION: <unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/057,009
 ; FILING DATE: 1998-04-07
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fasse, J. Peter
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 07917/010001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 668 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: No.
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-09-761-569-13

Query Match 35.0%; Score 606; DB 10; Length 668;
 Best Local Similarity 37.3%; Pred. No. 1.1e-45;
 Matches 141; Conservative 73; Mismatches 105; Indels 59; Gaps 12;

100

ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE KINASES

100

ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE KINASES

NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/761,569
 FILING DATE: 16-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/057,009
 FILING DATE: 1998-04-07
 ATTORNEY/AGENT INFORMATION:
 NAME: Fasse, J. Peter
 REGISTRATION NUMBER: 32,983
 REFERENCE/DOCKET NUMBER: 07917/010001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 400 amino acids
 TYPE: amino acid
 STRANDEDNESS: No. US20020102691A1 Relevant
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 US-09-761-569-12
 Query Match 32.7%; Score 566; DB 10; Length 400;
 Best Local Similarity 36.5%; Pred. No. 2e-42;
 Matches 125; Conservative 63; Mismatches 92; Indels 62; Gaps 8;

32 IDSKACISIGNONFEVAKADLEPIELGKAYGVEKMRHVPSCQIMAVKRIATVNSOE 91
 58 LIOKAKVS-----ELKDDDFERISELGAGNGVYTKVQHRPSGLIMARKLIHEIKPAI 111
 92 QKRLMDLDSMTVDCPTVTFYGFALFREGDWICMELMD-TSIDKRYKQVIDKQITP 150
 112 RQOIIELOY-LHECNSPYIVGYGAFYSGEISICMHHMDGSLD---QVLKAKRIP 166
 151 EDLGRKIASIVALEHLHSKLSVIHRDVKPSNVNLALGOVKMCDFGISGYLVDSYAKT 210
 167 EELTGKVSIAVLGLAVLRKHQIMHRDVKPSNLIIVNSRGEIKLDFGVSGQLIDSMANS 226
 211 IDAGCKPYMAPERINPELNOKGYSKSDIWSIGITMELAILRFPYDS-----WGT 261
 227 F-VGTRSYMAPER---LQGTHTSVQSDIWSMGLSLVELAVGRYPIPPDAKELFAIFGR 281
 262 P-----FOOLKQVVEEPPOLPADKFSAE 285
 282 PVDVGEGERPHSISPRPRPGRPVSGHGMDSRPMAIFELLDYIYNEPPKLPNGVFTPD 341
 286 FVDFTSQCLTKNSKERPTYPELMQHPFTLHESKGTDVASFV 327
 342 FOEFVNCKLIKPAERADLKMLTNHTFIKRSEVEEYDFAGWL 383

RESULT 15
 US-09-755-665-34
 Sequence 34, Application US/09755665
 Patent No. US20020107186A1
 GENERAL INFORMATION:
 APPLICANT: Prayaga, Sudhirdas K.
 APPLICANT: Majumder, Kumud

APPLICANT: Tallon, Bruce E.
 APPLICANT: Spaderna, Steven K.
 APPLICANT: Spylek, Kimberly A.
 APPLICANT: MacDougall, John
 TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 15966-631
 CURRENT APPLICATION NUMBER: US/09/755,665
 CURRENT FILING DATE: 2001-08-14
 PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
 PRIOR FILING DATE: 2000-01-06
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: Patentln Ver. 2.1
 SEQ ID NO 34
 LENGTH: 395
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-755-665-34
 Query Match 32.5%; Score 563; DB 10; Length 395;
 Best Local Similarity 36.9%; Pred. No. 3.7e-42;
 Matches 121; Conservative 62; Mismatches 89; Indels 56; Gaps 7;

46 EVKADLEPIELGKAYGVEKMRHVPSCQIMAVKRIATVNSOEQKRLMDLDSMT 105
 66 ELKDDDFERISELGAGNGVYTKVQHRPSGLIMARKLIHEIKPAIRQOIIELOY-LHE 124
 106 VDCPTVTFYGFALFREGDWICMELMD-TSIDKRYKQVIDKQITPEDIKIASIYKA 164
 125 CNSPYIVGYGAFYSDEISICMHHMDGSLD---QVLKAKRIPEDILKVSIAVLRG 180
 165 LEHLHSKLSVIHRDVKPSNVNLALGOVKMCDFGISGYLVDSYAKTIDAGCKPYMAPERI 224
 181 LAYLRKHQIMHRDVKPSNLIIVNSRGEIKLDFGVSGQLIDSMANSF-VGTRSYMAPER- 238
 225 NPELNOKGYSKSDIWSIGITMELAILRFPYDS-----WGT----- 262
 239 ---LQGTHTSVQSDIWSMGLSLVELAVGRYPIPPDAKELFAIFRPVYDGEGERPHSIS 295
 263 -----FOOLKQVVEEPPOLPADKFSAEVDFTSQCLTKNSK 299
 296 PRPRPGRPVSGHGMDSRPMAIFELLDYIYNEPPKLPNGVFTPDFOEFVNCKLIKPA 355
 300 ERPTYPELMQHPFTLHESKGTDVASFV 327
 356 ERADLKMLTNHTFIKRSEVEEYDFAGWL 383

Search completed: June 6, 2003, 09:17:20
 Job time : 50 secs

PT Mitogen-activated protein kinase kinase and corresponding DNA -
 PT phosphotyrosine p38 cascade members, used in the treatment of
 PT immunological-related cell proliferative diseases

Claim 1: Page 31-33; 67pp; English.

Human mitogen-activated protein kinase kinase MEK6 (AAW06319) is a
 CC protein capable of modulating the activity of the mitogen-activated
 CC protein kinase p38 (esp. p38-2). Its amino acid sequence was
 CC deduced from a cDNA clone (AA068716) obtd. from a MOLT-4 cDNA
 CC library. MEK6 is 88% identical to its closest homologue MKK3,
 CC and all relevant kinase subdomains are conserved. MEK6
 CC polypeptides can be produced in transformed or transfected host
 CC cells. MEK6 and its variants, antibodies raised against MEK6, and
 CC MEK6 nucleic acids can be used to modulate (stimulate or inhibit)
 CC phosphorylation of p38 by MEK6 for use in the treatment of diseases
 CC associated with the p38 cascade e.g. immunological-related cell
 CC proliferative diseases and autoimmune diseases, and also to detect
 CC MEK6 kinase activity and identify proteins that interact with MEK6.

SO Sequence 334 AA:

Query Match 100.0%; Score 1731; DB 18; Length 334;
 Best Local Similarity 100.0%; Pred. No. 3.8e-163;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SOSKGRKRPGLKIPKEAFEPOTSSPPRLDLSKACISIGNONFEVKADDEPIMELGR 60
 DB 2 SOSKGRKRPGLKIPKEAFEPOTSSPPRLDLSKACISIGNONFEVKADDEPIMELGR 61
 OY 61 GAYGVEMKRNHVPSSQIMAVKRIRATVNSQEQRLMDLDSMRVDCPTVTFYDALFR 120
 DB 62 GAYGVEMKRNHVPSSQIMAVKRIRATVNSQEQRLMDLDSMRVDCPTVTFYDALFR 121
 OY 121 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIRHDKV 180
 DB 122 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIRHDKV 181
 OY 181 PSNVLLNALGOVAKMDFGIGSYLVDSVAKTIDAGCKPYMAPERINPELNQKGSVKSIDIW 240
 DB 182 PSNVLLNALGOVAKMDFGIGSYLVDSVAKTIDAGCKPYMAPERINPELNQKGSVKSIDIW 241
 OY 241 SLGITMIELAILRFPYDSWGTTPFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKNSKE 300
 DB 242 SLGITMIELAILRFPYDSWGTTPFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKNSKE 301
 OY 301 RPTYPELMQHPFTLHESKGTDVASFVKLLIGD 333
 DB 302 RPTYPELMQHPFTLHESKGTDVASFVKLLIGD 334

RESULT 2

AAW06319 standard; Protein; 334 AA.

AC AAW06319;

DT 07-FEB-1997 (first entry)

DE Human mitogen-activated protein kinase 6.

XX Mitogen-activated protein kinase kinase 6; MKK6; MAP;
 KW tyrosine kinase; signal transduction; cytokine; oncoprotein;
 KW stress; diagnosis; therapy.

XX Homo sapiens.

XX WO9636642-A1.

XX 21-NOV-1996.

XX 26-JAN-1996; 96WO-US01078.

PR 19-SEP-1995; 95US-0530950.
 PR 19-MAY-1995; 95US-0446083.

PA (DAVI/) DAVIS R J.
 PA (DERI/) DERIJARD B.
 PA (GUPT/) GUPTA S.
 PA (RAIN/) RAINGEAUD J.

PI Davis RJ, Derijard B, Gupta S, Raingeaud J;

DR WPI: 1997-012035/01.

DR N-PSDB; AAT43204.

PT New mitogen activated protein kinase kinase - useful for treating
 PT ischaemic heart disease, kidney failure etc., also for identifying
 PT modulators for treatment of similar conditions

PS Claim 6; Fig 5; 104pp; English.

Novel human mitogen activated protein kinase kinase 6 (MKK6)
 CC (AAW06319) has serine, threonine and tyrosine kinase activity, and
 CC mediates a signal transduction pathway that activates human
 CC mitogen-activated protein kinase (MAP) kinase p38. Its amino acid
 CC sequence was deduced from a cDNA clone (AA043204) obtd. from a human
 CC skeletal muscle library. Recombinant MKK6 can be produced in
 CC transformed host cells. MKK6 (AAW06318-22) are useful in the
 CC treatment of MKK-related disorders, e.g. ischaemic heart disease
 CC and kidney failure, for identifying modulators of MKK activity,
 CC and for raising antibodies.

SO Sequence 334 AA:

Query Match 100.0%; Score 1731; DB 18; Length 334;
 Best Local Similarity 100.0%; Pred. No. 3.8e-163;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SOSKGRKRPGLKIPKEAFEPOTSSPPRLDLSKACISIGNONFEVKADDEPIMELGR 60
 DB 2 SOSKGRKRPGLKIPKEAFEPOTSSPPRLDLSKACISIGNONFEVKADDEPIMELGR 61
 OY 61 GAYGVEMKRNHVPSSQIMAVKRIRATVNSQEQRLMDLDSMRVDCPTVTFYDALFR 120
 DB 62 GAYGVEMKRNHVPSSQIMAVKRIRATVNSQEQRLMDLDSMRVDCPTVTFYDALFR 121
 OY 121 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIRHDKV 180
 DB 122 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIRHDKV 181
 OY 181 PSNVLLNALGOVAKMDFGIGSYLVDSVAKTIDAGCKPYMAPERINPELNQKGSVKSIDIW 240
 DB 182 PSNVLLNALGOVAKMDFGIGSYLVDSVAKTIDAGCKPYMAPERINPELNQKGSVKSIDIW 241
 OY 241 SLGITMIELAILRFPYDSWGTTPFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKNSKE 300
 DB 242 SLGITMIELAILRFPYDSWGTTPFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKNSKE 301
 OY 301 RPTYPELMQHPFTLHESKGTDVASFVKLLIGD 333
 DB 302 RPTYPELMQHPFTLHESKGTDVASFVKLLIGD 334

RESULT 3

AAW97669 standard; Protein; 334 AA.

AC AAW97669;

DT 10-MAY-1999 (first entry)

DE Human mitogen activated protein kinase MKK6.

XX MKK6; mitogen activated protein kinase kinase; MAP kinase kinase;
 KW human; signal transduction; inflammation; psoriasis; AIDS; cancer;

KW apoptosis; therapy.
 XX Homo sapiens.
 OS
 XX MO9902547-A1.
 XX
 PD 21-JAN-1999.
 XX
 PF 07-JUL-1998; 98WO-US14101.
 XX
 PR 07-JUL-1997; 97US-0888429.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 PI Davis RJ, Tournier C, Whitmarsh A;
 DR WPI; 1999-120771/10.
 DR N-PSDB; AAX07066.
 XX
 PT New isolated mitogen-activated protein kinase isoforms - used
 PT to develop products for treating e.g. inflammatory disorders,
 PT oxidative damage, proliferative disorders or autoimmune disorders
 XX
 PS Disclosure; Page 129; 168pp; English.
 XX
 CC This polypeptide comprises human mitogen activated protein (MAP)
 CC kinase kinase 6 (MKK6). The amino acid sequence was deduced from an
 CC isolated human skeletal muscle cDNA clone (see AAX07066) and shows
 CC high homology to human MKK3 (see AAW97668). The human MAP kinase
 CC kinases MKK3, MKK4, MKK6 and MKK7 (see AAW97664 and AAW97668-72),
 CC described in the invention, mediate the transduction of specific
 CC signals from the cell surface to the nucleus along specific
 CC pathways. They are useful for screening reagents which modulate
 CC MKK activity. Such agents can be used to prevent or treat
 CC MKK-mediated disorders, e.g. inflammation, oxidative damage or
 CC stress-related proliferative disorders, e.g. psoriasis, AIDS,
 CC malignancies of e.g. the skin, bone marrow, lung, liver, breast,
 CC gastrointestinal system and genito-urinary tract. Agents which
 CC inhibit the activity or expression of MKK inhibit cell growth or
 CC cause apoptosis. MKK7 polynucleotides (see AAX07059-64) and
 CC polypeptides (see AAW97662-67) are claimed.
 XX
 SQ Sequence 334 AA;
 Query Match 100.0%; Score 1731; DB 20; Length 334;
 Best Local Similarity 100.0%; Pred. No. 3, 8e-163;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOSKGRKRNPGIKIPKEAFEPQTSSTPPRDLDSKACISIGNONFEVKADLEPIIMELGR 60
 DB 2 SOSKGRKRNPGIKIPKEAFEPQTSSTPPRDLDSKACISIGNONFEVKADLEPIIMELGR 61
 QY 61 GAYGVVKMRHVPSCQIMAVKRIKATVNSQEQRLMDLISMRTVDCPTVTFYALFR 120
 DB 62 GAYGVVKMRHVPSCQIMAVKRIKATVNSQEQRLMDLISMRTVDCPTVTFYALFR 121
 QY 121 EGDVWICMELMDTSLDKFYKQVIDKQGTIPEDILGKIAVSIKALEHLSKLSYIHRDV 180
 DB 122 EGDVWICMELMDTSLDKFYKQVIDKQGTIPEDILGKIAVSIKALEHLSKLSYIHRDV 181
 QY 181 PSNVLLINALGOVKMCDPFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 240
 DB 182 PSNVLLINALGOVKMCDPFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 241
 QY 241 SLGITMIELALIRFPYDSNGTPEQOLKQVVEEPSQOLPADKFSAEFVDFTSQCLKNKSKE 300
 DB 242 SLGITMIELALIRFPYDSNGTPEQOLKQVVEEPSQOLPADKFSAEFVDFTSQCLKNKSKE 301
 QY 301 RPTYPELMQHPFFTLHESKGTDVASFVKLLIGD 333
 DB 302 RPTYPELMQHPFFTLHESKGTDVASFVKLLIGD 334

RESULT 4
 AAY57392
 ID AAY57392 standard; Protein: 334 AA.
 XX
 AC AAY57392;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Human MAPK kinase 6 polypeptide.
 XX
 KW Mitogen-activated protein kinase; MAPK; MAPK kinase 6; antisense;
 KW sandwich assay; human.
 XX
 OS Homo sapiens.
 XX
 PN US6033910-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 19-JUL-1999; 99US-0357073.
 XX
 PR 19-JUL-1999; 99US-0357073.
 XX
 PA (ISIS-) ISIS PHARM INC.
 PI Monia BP, Cowsett LM;
 DR WPI; 2000-269479/23.
 DR N-PSDB; AAZ98598.
 XX
 PT Novel antisense oligonucleotides used for inhibition of
 PT Mitogen-activated protein kinase kinase 6 expression -
 XX
 PS Example 13; Columns 45-50; 33pp; English.
 XX
 CC The invention provides antisense oligonucleotides which are targeted to a
 CC nucleic acid encoding a mitogen-activated protein kinase (MAPK) kinase 6.
 CC The antisense oligonucleotides are used to inhibit MAPK kinase 6
 CC expression, and so are used to treat diseases mediated by MAPK kinase 6
 CC expression. They may also be used to detect MAPK kinase 6, e.g. in
 CC sandwich assays. The present sequence represents the human MAPK kinase 6.
 XX
 SQ Sequence 334 AA;
 Query Match 100.0%; Score 1731; DB 21; Length 334;
 Best Local Similarity 100.0%; Pred. No. 3, 8e-163;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOSKGRKRNPGIKIPKEAFEPQTSSTPPRDLDSKACISIGNONFEVKADLEPIIMELGR 60
 DB 2 SOSKGRKRNPGIKIPKEAFEPQTSSTPPRDLDSKACISIGNONFEVKADLEPIIMELGR 61
 QY 61 GAYGVVKMRHVPSCQIMAVKRIKATVNSQEQRLMDLISMRTVDCPTVTFYALFR 120
 DB 62 GAYGVVKMRHVPSCQIMAVKRIKATVNSQEQRLMDLISMRTVDCPTVTFYALFR 121
 QY 121 EGDVWICMELMDTSLDKFYKQVIDKQGTIPEDILGKIAVSIKALEHLSKLSYIHRDV 180
 DB 122 EGDVWICMELMDTSLDKFYKQVIDKQGTIPEDILGKIAVSIKALEHLSKLSYIHRDV 181
 QY 181 PSNVLLINALGOVKMCDPFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 240
 DB 182 PSNVLLINALGOVKMCDPFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 241
 QY 241 SLGITMIELALIRFPYDSNGTPEQOLKQVVEEPSQOLPADKFSAEFVDFTSQCLKNKSKE 300
 DB 242 SLGITMIELALIRFPYDSNGTPEQOLKQVVEEPSQOLPADKFSAEFVDFTSQCLKNKSKE 301
 QY 301 RPTYPELMQHPFFTLHESKGTDVASFVKLLIGD 333
 DB 302 RPTYPELMQHPFFTLHESKGTDVASFVKLLIGD 334

RESULT 5
 AAB31689
 ID AAB31689 standard; Protein: 334 AA.
 XX
 AC AAB31689;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE A human mitogen-activated protein kinase MKK6.
 XX
 KW Mitogen-activated protein kinase; MAP kinase kinase; MKK; MKK6;
 KW inflammation; oxidative damage; ischemic heart disease; burn; alcohol;
 KW kidney failure; liver damage; oxidative stress; rheumatoid arthritis;
 KW respiratory distress syndrome; septic shock; autoimmune disorder;
 KW inflammatory disease; proliferative disorder; psoriasis;
 KW acquired immune deficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN US6174676-B1.
 PD 16-JAN-2001.
 XX
 PF 08-SEP-1998; 98US-0149879.
 XX
 PR 07-APR-1998; 98US-0057009.
 PR 19-MAY-1995; 95US-0446083.
 PR 19-SEP-1995; 95US-0530950.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX
 PI Davis RJ, Ralngeaud J, Derijard B;
 XX
 DR WPI: 2001-181551/18.
 DR N-PSDB; AAF25239.
 XX
 PT Identifying mitogen-activating protein kinase activity (MKK), synthesis
 PT or expression modulators, comprises measuring effect of test reagent on
 PT MKK phosphorylation, synthesis or expression after incubation with MKK
 PT
 XX
 PT
 XX
 PS Disclosure: Fig 5A-C; 59pp; English.
 XX
 PS
 CC The present sequence represents a human mitogen-activated protein (MAP)
 CC kinase kinase MKK6. The specification describes a method for identifying
 CC a reagent that modulates mitogen-activating MAP kinase kinase (MKK)
 CC activity, synthesis or expression. The method comprises incubating MKK
 CC with the test reagent and measuring the effect of the test reagent on
 CC phosphorylation, MKK synthesis or MKK expression. MKK modulating reagents
 CC identified by the method of the invention are useful for treating or
 CC preventing MKK mediated disorders such as inflammation, oxidative damage,
 CC ischemic heart disease, burns due to heat or radiation, kidney failure,
 CC liver damage due to oxidative stress or alcohol, respiratory distress,
 CC syndrome, septic shock, rheumatoid arthritis, autoimmune disorders, and
 CC other types of inflammatory diseases and stress-related MKK-mediated
 CC proliferative disorders such as psoriasis, acquired immune deficiency
 CC syndrome, malignancies of various tissues of the body, including
 CC malignancies of the skin, bone marrow, lung, liver, breast etc..
 CC
 XX
 SQ Sequence 334 AA;
 Query Match 100.0%; Score 1731; DB 22; Length 334;
 Best Local Similarity 100.0%; Pred. No. 3,8e-163; Indels 0; Gaps 0;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOSGKRRNPEGLKPKKEAFEPQRTSTPPRDLDSKACISIGNONFEVAKADLEPIIMELGR 60
 DB 2 SOSGKRRNPEGLKPKKEAFEPQRTSTPPRDLDSKACISIGNONFEVAKADLEPIIMELGR 61
 QY 61 GAGGVVKKMRVPSGQIMAVKRIRATVNSQOKRLMDLDIMSKRVDCPFYTFGALFR 120
 DB 62 GAGGVVKKMRVPSGQIMAVKRIRATVNSQOKRLMDLDIMSKRVDCPFYTFGALFR 121

QY 121 EGDWICMEIMDTSIDKFPKQYIDKGQRTIPEDILGKIAVSIYKALEHLSKLSVIRHDK 180
 DB 122 EGDWICMEIMDTSIDKFPKQYIDKGQRTIPEDILGKIAVSIYKALEHLSKLSVIRHDK 181
 QY 181 PSNVILNAGVKMCDGFSIGYLVDSVAKTIDAGCKPYMAPRINPELNQKGSVSDIM 240
 DB 182 PSNVILNAGVKMCDGFSIGYLVDSVAKTIDAGCKPYMAPRINPELNQKGSVSDIM 241
 QY 241 SLGTTMELALIRFSDYDWSGTPFQOLKQVEEPSQOLPADKSAEVDFTSQCLKNKSE 300
 DB 242 SLGTTMELALIRFSDYDWSGTPFQOLKQVEEPSQOLPADKSAEVDFTSQCLKNKSE 301
 QY 301 RPTYPELMQHPFFTLHESKGTDVASFVKLIIGD 333
 DB 302 RPTYPELMQHPFFTLHESKGTDVASFVKLIIGD 334
 RESULT 6
 ABG07309
 ID ABG07309 standard; Protein: 267 AA.
 XX
 AC ABG07309;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #7300.
 XX
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HXSFQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS71496.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PT
 XX
 PS Claim 20; SEQ ID NO 37668; 103pp; English.
 CC
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 267 AA:

Query Match 80.2%; Score 1389; DB 22; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.5e-129;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 67 EKMRRVPSGQIMAVKRRIRATVNSQOKRLMDLDMISMRVDCFTVTFYGFALREGDWT 126
DB 1 EKMRRVPSGQIMAVKRRIRATVNSQOKRLMDLDMISMRVDCFTVTFYGFALREGDWT 60
QY 127 CMEIMDTSIDKFKYKVIDKGOTIPEDILGKIAVSYKALEHLSKTSVYHRDVKPSNVLI 186
DB 61 CMEIMDTSIDKFKYKVIDKGOTIPEDILGKIAVSYKALEHLSKTSVYHRDVKPSNVLI 120
QY 187 NALGOVKMCDGFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDWISLIGITM 246
DB 121 NALGOVKMCDGFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDWISLIGITM 180
QY 247 IELALIRFPYDSWGTGTPFOOLKQVVEPSPOLPADKFSAEFVDTFSQCLKNKSKERTYPE 306
DB 181 IELALIRFPYDSWGTGTPFOOLKQVVEPSPOLPADKFSAEFVDTFSQCLKNKSKERTYPE 240
QY 307 LMOHPFTLHESKGTDVASFVKLLIGD 333
DB 241 LMOHPFTLHESKGTDVASFVKLLIGD 267

```

RESULT 7

ID ABG12149 standard; Protein; 359 AA.

AC ABG12149;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #12140.

KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW Food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS76336.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 20; SEQ ID No 42508; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

Sequence 359 AA:

Query Match 80.0%; Score 1384; DB 22; Length 359;
Best Local Similarity 80.2%; Pred. No. 1.2e-128;
Matches 267; Conservative 33; Mismatches 31; Indels 2; Gaps 2;

```

QY 2 QSKGK-KRNGKIKPKAEFEPOTSSTPPRLDSKACISIGNONFEVADLIEPIMEIGR 60
DB 26 QSKGSKRRKRDRLSCMS-KPPAPNPPPPRLDSRTFTTIDRNEVEADLVITSEIGR 84
QY 61 GAYGVVEKMRHVPSGQIMAVKRRIRATVNSQOKRLMDLDMISMRVDCFTVTFYGFALFR 120
DB 85 GAYGVVEKMRHVPSGQIMAVKRRIRATVNSQOKRLMDLDMISMRVDCFTVTFYGFALFR 144
QY 121 EGDVWICMEIMDTSIDKFKYKVIDKGOTIPEDILGKIAVSYKALEHLSKTSVYHRDVK 180
DB 145 EGDVWICMEIMDTSIDKFKYKVIDKGOTIPEDILGKIAVSYKALEHLSKTSVYHRDVK 204
QY 181 PSNVLLNALGOVKMCDGFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDW 240
DB 205 PSNVLLINKESGVKMKCDGFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDW 264
QY 241 SLGITMIELALIRFPYDSWGTGTPFOOLKQVVEPSPOLPADKFSAEFVDTFSQCLKNKSK 300
DB 265 SLGITMIELALIRFPYDSWGTGTPFOOLKQVVEPSPOLPADKFSAEFVDTFSQCLKNKSK 324
QY 301 RPTYPELMOHPFTLHESKGTDVASFVKLLIGD 333
DB 325 RPTYPELMOHPFTLHESKGTDVASFVKLLIGD 357

```

RESULT 8

ID AAM06318 standard; Protein; 318 AA.

AC AAM06318;

DT 07-FEB-1997 (first entry)

DE Human mitogen-activated protein kinase 3.

KW Mitogen-activated protein kinase 3; MKK3; MAP;
KW Tyrosine kinase; signal transduction; cytokine; oncoprotein;
KW stress; diagnosis; therapy.

OS Homo sapiens.

PN WO9636642-A1.

PD 21-NOV-1996.

PR 26-JAN-1996; 96WO-US01078.

PR 19-SEP-1995; 95US-0530950.
PR 19-MAY-1995; 95US-0446083.

XX (DAVI/) DAVIS R J.
 PA (DERI/) DERIJARD B.
 PA (GUPT/) GUPTA S.
 PA (RAIN/) RAINGAUD J.
 XX Davis RJ, Derijard B, Gupta S, Raingaud J;
 XX WPI: 1997-012035/01.
 DR N-PSDB: AAT43203.
 XX New mitogen activated protein kinase kinase - useful for treating
 PT ischaemic heart disease, kidney failure etc., also for identifying
 PT modulators for treatment of similar conditions
 XX
 XX Claim 2: Fig 4; 104pp: English.
 XX
 CC Novel human mitogen activated protein kinase kinase 3 (MKK3)
 CC (AAW06318) has serine, threonine and tyrosine kinase activity, and
 CC mediates a signal transduction pathway that activates human
 CC mitogen-activated protein (MAP) kinase p38. Its amino acid
 CC sequence was deduced from a cDNA clone (AAT43203) obtd. from a human
 CC foetal brain library. MKK3 is expressed in all tissues tested, but
 CC partic. in skeletal muscle. Recombinant MKK3 can be produced in
 CC transformed host cells. MKK3 (AAW06318-22) can be used in the
 CC treatment of MKK-related disorders, e.g. ischaemic heart disease
 CC and kidney failure, to identify modulators of MKK activity, and
 CC to raise antibodies.
 CC
 XX Sequence 318 AA:
 SO
 Query Match 79.0%; Score 1367; DB 18; Length 318;
 Best Local Similarity 82.7%; Pred. No. 4,8e-127;
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;
 QY 22 POTSSTPRDLDSKACISIGNONFEVKADLEPIELGKAYGVKRRHVPSCQIMAVK 81
 DB 5 PAVNPPTPRNLDSTRTFTITIGDRNFEVADLVITISELGRGAYGVKRRHVSQTIMAVK 64
 QY 82 RIRATVNSOQKRLMDLIDISMTVDCPFTVTFYGFALFRGQDWICHELMDTSLDKFYKQ 141
 DB 65 RIRATVNSOQKRLMDLIDISMTVDCPFTVTFYGFALFRGQDWICHELMDTSLDKFYRK 124
 QY 142 VIDKQTIPEIDILGKIAVSIKALEHLSKLSYIHRDVKPSNVNLINALGQVKMCDPFGISG 201
 DB 125 VIDKNTIPEIDILGKIAVSIKALEHLSKLSYIHRDVKPSNVNLINKGHVKMCDPFGISG 184
 QY 202 YLVDSVAKTIDAGCKPYMAERINPELNQKGYSVKSDIWSIGTMIETAILRPPYDSMGT 261
 DB 185 YLVDSVAKTIDAGCKPYMAERINPELNQKGYSVKSDIWSIGTMIETAILRPPYDSMGT 244
 QY 262 PFOOLKQVVEEPPQLPADKFSAEFVDFTSQCLKKNSEKRPPTYBELMQHPFTLHESKGT 321
 DB 245 PFOOLKQVVEEPPQLPADKFSAEFVDFTSQCLKKNSEKRPPTYBELMQHPFTLHESKGT 304
 QY 322 DVASFVKLLIGD 333
 DB 305 DIAAFVKKILGE 316
 RESULT 9
 AAW97668 standard; Protein; 318 AA.
 ID AAW97668;
 AC AAW97668;
 DT 10-MAY-1999 (first entry)
 XX Human mitogen activated protein kinase kinase MKK3.
 DE Human mitogen activated protein kinase kinase MKK3.
 XX MKK3; mitogen activated protein kinase kinase; MAP kinase kinase;
 KW human; signal transduction; inflammation; psoriasis; AIDS; cancer;
 KW apoptosis; therapy.

XX Homo sapiens.
 OS
 XX WO9902547-A1.
 PN
 XX 21-JAN-1999.
 PD
 XX 07-JUL-1998; 98WO-US14101.
 PE
 XX 07-JUL-1997; 97US-0888429.
 FR
 XX (UYMA-) UNIV MASSACHUSETTS.
 PA Davis RJ, Tournier C, Whitmarsh A;
 XX WPI: 1999-120771/10.
 DR N-PSDB: AAX07065.
 DR
 XX New isolated mitogen-activated protein kinase kinase isoforms - used
 PT to develop products for treating e.g. inflammatory disorders,
 PT oxidative damage, proliferative disorders or autoimmune disorders
 XX
 XX Example 1: Page 126-127; 168pp: English.
 XX
 CC This polypeptide comprises human mitogen activated protein (MAP)
 CC kinase kinase 3 (MKK3), a 36 kDa protein that phosphorylates p38 but
 CC not JNK1 or ERK2. The amino acid sequence was deduced from an
 CC isolated human brain cDNA clone (see AAX07065). The human MAP kinase
 CC kinases MKK3, MKK4, MKK6 and MKK7 (see AAW97664 and AAW97668-72),
 CC described in the invention, mediate the transduction of specific
 CC signals from the cell surface to the nucleus along specific
 CC pathways. They are useful for screening reagents which modulate
 CC MKK activity. Such agents can be used to prevent or treat
 CC MKK-mediated disorders, e.g. inflammation, oxidative damage or
 CC stress-related proliferative disorders, e.g. psoriasis, AIDS,
 CC malignancies of e.g. the skin, bone marrow, lung, liver, breast,
 CC gastrointestinal system and genito-urinary tract. Agents which
 CC inhibit the activity or expression of MKK inhibit cell growth or
 CC cause apoptosis. MKK7 polynucleotides (see AAX07059-64) and
 CC polypeptides (see AAW97662-67) are claimed.
 CC
 XX Sequence 318 AA:
 SO
 Query Match 79.0%; Score 1367; DB 20; Length 318;
 Best Local Similarity 82.7%; Pred. No. 4,8e-127;
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;
 QY 22 POTSSTPRDLDSKACISIGNONFEVKADLEPIELGKAYGVKRRHVPSCQIMAVK 81
 DB 5 PAVNPPTPRNLDSTRTFTITIGDRNFEVADLVITISELGRGAYGVKRRHVSQTIMAVK 64
 QY 82 RIRATVNSOQKRLMDLIDISMTVDCPFTVTFYGFALFRGQDWICHELMDTSLDKFYKQ 141
 DB 65 RIRATVNSOQKRLMDLIDISMTVDCPFTVTFYGFALFRGQDWICHELMDTSLDKFYRK 124
 QY 142 VIDKQTIPEIDILGKIAVSIKALEHLSKLSYIHRDVKPSNVNLINALGQVKMCDPFGISG 201
 DB 125 VIDKNTIPEIDILGKIAVSIKALEHLSKLSYIHRDVKPSNVNLINKGHVKMCDPFGISG 184
 QY 202 YLVDSVAKTIDAGCKPYMAERINPELNQKGYSVKSDIWSIGTMIETAILRPPYDSMGT 261
 DB 185 YLVDSVAKTIDAGCKPYMAERINPELNQKGYSVKSDIWSIGTMIETAILRPPYDSMGT 244
 QY 262 PFOOLKQVVEEPPQLPADKFSAEFVDFTSQCLKKNSEKRPPTYBELMQHPFTLHESKGT 321
 DB 245 PFOOLKQVVEEPPQLPADKFSAEFVDFTSQCLKKNSEKRPPTYBELMQHPFTLHESKGT 304
 QY 322 DVASFVKLLIGD 333
 DB 305 DIAAFVKKILGE 316
 RESULT 10

CC related diseases. The method of the invention comprises contacting a
 CC test compound with at least one of the cellular kinases RICK, RIK, RIKK,
 CC NCK-interacting kinase, MKK3 and SRPK-2 and detecting any change in
 CC kinase activity. The method of the invention can be used to treat and/or
 CC prevent CMV infections and related diseases. Oligonucleotides that can
 CC detect the specified kinases can also be used for diagnosis of infection.
 CC The present amino acid sequence represents the human cellular kinase MKK3
 CC protein of the invention, as described above.

XX Sequence 318 AA;

Query Match 79.0%; Score 1367; DB 23; Length 318;
 Best Local Similarity 82.7%; Pred. No. 4,8e-127;
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;

QY 22 POTSSTPRDLDSKACISIGNONFEVKADLDLEPIMELGAGAVYKRMHVPSCGMAYK 81
 Db 5 PAPNTPPRNDSKRTFTIGDNRFEADDLVTISELGGAGVYKRVHQAOSGTLMAVK 64
 QY 82 RIRATVNSQEQKRLMDLIDSMRTVDCPTVTYFGALFREGDWMICMELMDTSLDKFYKQ 141
 Db 65 RIRATVNSQEQKRLMDLIDSMRTVDCPTVTYFGALFREGDWMICMELMDTSLDKFYK 124
 QY 142 VIDGORTPEIDILGIAVSIYKALEHLSKLSVHRDVKPSNVLLNALGVKMGDFGIGS 201
 Db 125 VLDRNMFTPEIDILGIAVSIYKALEHLSKLSVHRDVKPSNVLLNALGVKMGDFGIGS 184
 QY 202 YLVDSVAKTIDAGCKPYAPERINPELNOKGYSKSDIWSLGITMIELALPEPYDSMGT 261
 Db 185 YLVDSVAKTMDAGCKPYAPERINPELNOKGYNKSDIWSLGITMIELALPEPYDSMGT 244
 QY 262 PFQOLKQVEPSPQOLPADKFSAEFVDTSCCLKNKSERPTYPELMOHPEFTLHESKGT 321
 Db 245 PFQOLKQVEPSPQOLPADKFSAEFVDTSCCLKNKSERPTYPELMOHPEFTLHESKGT 304
 QY 322 DVASFVKLLIGD 333
 Db 305 DIAAFVKLLIGE 316

RESULT 14
 ABG23442

ID ABG23442 standard; Protein; 359 AA.

AC ABG23442;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #23433.

KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-0508631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSF-) HYSFQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

XX N-PSDB; AAS87629.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

Claim 20; SEQ ID No 53801; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 359 AA;

Query Match 74.8%; Score 1295; DB 22; Length 359;
 Best Local Similarity 76.0%; Pred. No. 8.1e-120;
 Matches 253; Conservative 35; Mismatches 43; Indels 2; Gaps 2;

QY 2 QSKGK-KRNGCLKIPKAFEPQOTSPPRDLDSKACISIGNONFEVKADLDLEPIMEGR 60
 Db 26 QSKGSKRRKKDLRISCMS-KPAPNTPPRNLDSTFTIGDNRFEADDLVTISELGR 84
 QY 61 GAYGVYKMRHVPSCGMAYKRIATVNSQEQKRLMDLIDSMRTVDCPTVTYFGALFR 120
 Db 85 GAYGVYKRVHQAOSGTLMAVKRIATVNSQEQKRLMDLIDSMRTVDCPTVTYFGALFR 144
 QY 121 EGDVWICMELMDTSLDKFYKQVIDKGQITPEIDILGIAVSIYKALEHLSKLSVHRDVK 180
 Db 145 EGDVWICMELMDTSLDKFYKQVIDKGQITPEIDILGIAVSIYKALEHLSKLSVHRDVK 204
 QY 181 PSNVLLNALGVKMGDFGIGSGLYDVAKTIDAGCKPYAPERINPELNOKGYSKSDI 240
 Db 205 PSNVLLNALGVKMGDFGIGSGLYDVAKTIDAGCKPYAPERINPELNOKGYSKSHW 264
 QY 241 SIGITMIELALPEPYDSMGTPEQOLKQVEPSPQOLPADKFSAEFVDTSCCLKNKSKE 300
 Db 265 SIGITMIELALPEPYDSMGTPEQOLKQVEPSPQOLPADKFSAEFVDTSCCLKNKP 324
 QY 301 RPTYPELMOHPEFTLHESKGTDVASFVKLLIGD 333
 Db 325 RMSYLEIMEHPFTLHESKGTDVASFVKLLIGE 357

RESULT 15

ID ABB57326 standard; Protein; 237 AA.

AC ABB57326;

DT 07-MAR-2002 (first entry)

DE Mouse ischemic condition related protein sequence SEQ ID NO:907.

KM Mouse; ischemia; compressive ischemia; occlusive ischemia;

KW vasospastic ischemia; ischemic condition; ischemic disease.

XX Mus musculus.

PN WO20018188-A2.

XX 22-NOV-2001.

PD 18-MAY-2001; 2001WO-JP04192.

XX 18-MAY-2001; 2000JP-0145977.

PR 18-MAY-2000; 2000JP-0145977.

XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

DR N-PSDB; AB199801.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -

PS Claim 2; Page 2293-2294; 2690pp; English.

XX The present invention describes a method for examining ischemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischemic condition (e.g. compressive
CC ischemia, occlusive ischemia or vasospastic ischemia) by measuring
CC expression levels of particular genes (AB199202 to AB199912, encoding
CC the protein sequences in AB57020 to AB57374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischemic condition-improving
CC drugs or therapeutics for ischemic diseases. AB199913 and AB199914
CC represent PCR primers for a mouse ischemic condition related sequence,
CC which are used in the exemplification of the present invention.

XX SQ Sequence 237 AA;

Query Match 70.5%; Score 1221; DB 23; Length 237;

Best Local Similarity 97.5%; Pred. No. 9.9e-113; Indels 0; Gaps 0;

Matches 231; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 97 MDLDSMRTVDCPFTVTFYGFALFREGDVWICMELMDTSLDKFYKQVIDKGOTIPEDILGK 156

Db 1 MDLDSMRTVDCPFTVTFYGFALFREGDVWICMELMDTSLDKFYKQVIDKGOTIPEDILGK 60

OY 157 IAVSIVAKLEHLHSLKLSYIHRDVKPSNVLINALGOVKMCDGIGSYLDVSAKTIIDAGCK 216

Db 61 IAVSIVAKLEHLHSLKLSYIHRDVKPSNVLINALGOVKMCDGIGSYLDVSAKTIIDAGCK 120

OY 217 PYMAPERINPELNOKGYSVKSDISLIGTMTIELALRPYPDSWGTFFOOLKQVVEPSPQ 276

Db 121 PYMAPERINPELNOKGYSVKSDISLIGTMTIELALRPYPDSWGTFFOOLKQVVEPSPQ 180

OY 277 LPADKFSAEFVDFTSQCLKKNKSKERTYPELMOHPFTLHESKGTIVASFKVLLIGD 333

Db 181 LPADKFSAEFVDFTSQCLKKNKSKERTYPELMOHPFTLHESKGTIVASFKVLLIGD 237

Search completed: June 6, 2003, 09:10:29
Job time : 73 secs

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OM protein - protein search, using sw model

Run on: June 6, 2003, 09:07:33 ; Search time 19 Seconds

(without alignments)
1684.882 Million cell updates/sec

Title: US-09-593-288-2

Perfect score: 1731

Sequence: 1 SOSGKRRNPGLKIPKEAFE.....TTHESKGTDVASFVKLLGD 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1731	100.0	334	2	S71631
2	1705	98.5	334	2	S71632
3	1367	79.0	318	2	A55556
4	924.5	53.4	445	2	S36039
5	922.5	53.3	457	2	A54694
6	919	53.1	399	2	I38901
7	882	51.0	395	2	S52423
8	865.5	50.0	345	2	T16665
9	822	47.5	162	2	S71633
10	628.5	36.3	363	2	T22107
11	618	35.7	359	2	T26025
12	610.5	35.3	605	2	T16583
13	607.5	35.1	605	2	S18648
14	606	35.0	668	2	S56909
15	587	33.9	393	1	A45100
16	587	33.9	393	1	JN0840
17	586.5	33.9	393	1	I59571
18	586.5	33.9	401	1	I52829
19	586	33.9	393	1	SA2068
20	583	33.7	400	1	AA8081
21	572	33.2	395	1	S36186
22	572	33.2	393	1	S41054
23	565	32.6	397	1	S41054
24	563	32.5	400	1	AA6723
25	560	32.4	1218	2	T29915
26	552	31.9	444	2	A56708
27	541	31.3	393	1	AA5176
28	525	30.3	387	1	A56466
29	508.5	29.4	435	2	T37324

ALIGNMENTS

RESULT 1

S71631

mitogen-activated protein kinase kinase (EC 2.7.1.-) 6 [similarity] - human

N:Alternate names: MAP kinase kinase SAPK3

C:Species: Homo sapiens (man)

C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 08-Sep-2000

C:Accession: S71631; A59347

R:Cuenda, A.; Alonso, G.; Morrice, N.; Jones, M.; Meier, R.; Cohen, P.; Nebreda, A.

EMBO J. 15, 4156-4164, 1996

A:Title: Purification and cDNA cloning of SAPK3, the major activator of RK/p38 in

A:Reference number: S71631; MUID:97015116; PMID:8861944

A:Accession: S71631

A:Molecule type: mRNA

A:Residues: 1-334 <CUE>

A:Cross-references: EMBL:X6757; NID:g1495484; PIDN:CA65532.1; PID:g1495485

A:Experimental source: cell type B cell; cell line BUB

J.Han, J.; Lee, J.D.; Jiang, Y.; Li, Z.; Peng, L.; Ulevitch, R.J.

J. Biol. Chem. 271, 2886-2891, 1996

A:Title: Characterization of the structure and function of a novel MAP kinase kinas

A:Reference number: A59347; MUID:96216353; PMID:8621675

A:Accession: A59347

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>

A:Cross-references: GB:039064; NID:g1209670; PIDN:AA03708.1; PID:g1209671

C:Gene: GDB:MAP2K6; PRKMK6; MEK6; MKK6; SAPK3

A:Cross-references: GDB:1230470; OMIM:601254

C:Superfamily: Kinase-related transforming protein; protein kinase homology

C:Keywords: Arp; phosphotransferase

F:51-314/Domain: protein kinase homology <KIN>

F:59-67/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 100.0%; Score 1731; DB 2; Length 334;

Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SOSGKRRNPGLKIPKEAFEQPTSSPPRLDSKACISIGNQNEVKAADLEPMEIGR 60

2 SOSGKRRNPGLKIPKEAFEQPTSSPPRLDSKACISIGNQNEVKAADLEPMEIGR 61

61 GAYGVKRMHVPESGOIMAYKRIATVNSOQKRLMDLDSMKRVDCPFYTFGALFR 120

62 GAYGVKRMHVPESGOIMAYKRIATVNSOQKRLMDLDSMKRVDCPFYTFGALFR 121

121 EGDVWICMEIMDSLDFYKQVNDKQTIPEIDIGKIAVSIVKALEHSHKLSVTHRYVK 180

122 EGDVWICMEIMDSLDFYKQVNDKQTIPEIDIGKIAVSIVKALEHSHKLSVTHRYVK 181

181 PSNVLINALGVKMKCPDGISGYLVDSVAKTIDACCKPYMAPERINPELNQKGYSVKSDIW 240

182 PSNVLINALGVKMKCPDGISGYLVDSVAKTIDACCKPYMAPERINPELNQKGYSVKSDIW 241

QY 241 SLGITMIELALIRPPYDSWGTSPFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKKSKE 300
 DB 242 SLGITMIELALIRPPYDSWGTSPFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKKSKE 301
 QY 301 RPTYPELMOHPEFTLHESKGTDAVSFKLLIGD 333
 DB 302 RPTYPELMOHPEFTLHESKGTDAVSFKLLIGD 334

RESULT 2

MAP kinase kinase (EC 2.7.1.-) SAPK3 isoform A - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Jun-2000
 C:Accession: S71632
 R:Cluend, A.; Alonso, G.; Morrice, N.; Jones, M.; Meler, R.; Cohen, P.; Nebreda, A.R.
 EMBO J. 15, 4156-4164, 1996
 A:Title: Purification and cDNA cloning of SAPK3, the major activator of RK/p38 in stress
 A:Reference number: S71631; MUID:97015116; PMID:8861944
 A:Accession: S71632
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-334 <CDS>
 A:Cross-references: EMBL:X97052; NID:q1495701; PIDN:CAA65764.1; PID:q1495702
 A:Experimental source: cell type fibroblast
 C:Genetics:
 A:Gene: SAPK3
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase
 F:51-314/Domain: protein kinase homology <KIN>
 F:59-67/Region: protein kinase ATP-binding motif

Query Match 98.5%; Score 1705; DB 2; Length 334;
 Best Local Similarity 97.9%; Pred. No. 3,3e-81;
 Matches 326; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 SOSGKRRRGKIKPEAFEPQSTSPREDLSKACISIGNQFEVKADLEPIIMELGR 60
 DB 2 SOSGKRRRGKIKPEAFEPQSTSPREDLSKACISIGNQFEVKADLEPIYELGR 61
 QY 61 GAYGVYKRRHVPSSGOIMAVKIRATVNSQEQRLMDLDSMRTVDCPTVTFYCALFR 120
 DB 62 GAYGVYKRRHVPSSGOIMAVKIRATVNSQEQRLMDLDSMRTVDCPTVTFYCALFR 121
 QY 121 EGDVWICMELMDSIDKFKYQVNDKQOTIPEDILGKAVSIKALEHLSKLSYIHRDV 180
 DB 122 EGDVWICMELMDSIDKFKYQVNDKQOTIPEDILGKAVSIKALEHLSKLSYIHRDV 181
 QY 181 PSNVLLNAGQVAKMCDGFSIGYLVDSYAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 240
 DB 182 PSNVLLNAGQVAKMCDGFSIGYLVDSYAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 241
 QY 241 SLGITMIELALIRPPYDSWGTSPFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKKSKE 300
 DB 242 SLGITMIELALIRPPYDSWGTSPFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKKSKE 301
 QY 301 RPTYPELMOHPEFTLHESKGTDAVSFKLLIGD 333
 DB 302 RPTYPELMOHPEFTLHESKGTDAVSFKLLIGD 334

RESULT 3

MAP kinase kinase (EC 2.7.1.-) 3 [similarity] - human
 A:Accession: A55556
 N:Alternate names: MAP kinase kinase 3 (MKK3)
 C:Species: Homo sapiens (man)
 C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 08-Sep-2000
 C:Accession: A55556
 R:Berjard, B.; Ringeaud, J.; Barrett, T.; Wu, I.H.; Han, J.; Ulevitch, R.J.; Davis, R.
 Science 267, 682-685, 1995
 A:Title: Independent human MAP kinase signal transduction pathways defined by MEK and MK
 A:Reference number: A55556; MUID:95141073; PMID:7839144

A:Accession: A55556
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-318 <EB>
 A:Cross-references: GB:L36719; NID:9685173; PIDN:AAQ41718.1; PID:9685174

C:Genetics:
 A:Gene: GDB:MAP2K3; PRKMK3; MEK3; MKK3
 A:Cross-references: GDB:9539640; OMIM:602315
 A:Map position: 17q11.2-17q11.2
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase
 F:33-296/Domain: protein kinase homology <KIN>
 F:41-49/Region: protein kinase ATP-binding motif

Query Match 79.0%; Score 1367; DB 2; Length 318;
 Best Local Similarity 82.7%; Pred. No. 7.8e-64;
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;

QY 22 POTSPPRDLDSKACISIGNQFEVKADLEPIIMELGRGAYGVYKRRHVPSSGOIMAVK 81
 DB 5 PARNPPRRMDSSTFTTIDRNEVEADLVITSEIGRGAYGVYKRRHVPSSGOIMAVK 64
 QY 82 RIRATVNSQEQRLMDLDSMRTVDCPTVTFYCALFRGQVWICMELMDSIDKFKY 141
 DB 65 RIRATVNSQEQRLMDLDSMRTVDCPTVTFYCALFRGQVWICMELMDSIDKFKY 124
 QY 142 VIDKQOTIPEDILGKAVSIKALEHLSKLSYIHRDVKPSNVLLNAGQVAKMCDGFSIG 201
 DB 125 VLDRNMRTIPEDILGKAVSIKALEHLSKLSYIHRDVKPSNVLLNAGQVAKMCDGFSIG 184
 QY 202 YLVDVSAKTMAGCKPYMAPERINPELNOKGYSVKSDIWSLGITMIELALIRPPYDSWGT 261
 DB 185 YLVDVSAKTMAGCKPYMAPERINPELNOKGYSVKSDIWSLGITMIELALIRPPYDSWGT 244
 QY 262 PFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKKSKEPRPTYPELMOHPEFTLHESGT 321
 DB 245 PFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKKSKEPRPTYPELMOHPEFTLHESGT 304
 QY 322 DVASFVKLLIGD 333
 DB 305 DIAAFVKLLIGD 316

RESULT 4

MAP kinase activator 2 - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-Dec-1997
 C:Accession: S36039
 R:Yashear, B.M.
 Submitted to the EMBL Data Library, May 1993.

A:Reference number: S36039
 A:Accession: S36039
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-445 <YAS>
 A:Cross-references: EMBL:222736
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
 F:146-413/Domain: protein kinase homology <KIN>
 F:154-162/Region: protein kinase ATP-binding motif

Query Match 53.4%; Score 924.5; DB 2; Length 445;
 Best Local Similarity 53.4%; Pred. No. 6.3e-41;
 Matches 183; Conservative 51; Mismatches 92; Indels 17; Gaps 5;

QY 1 SOSGKRRRGKIKPEAFEPQSTSPREDLSKACISIGNQFEVKADLEPIIMELGR 52
 DB 94 SYOKQLRPSGAKALSTNEQATKRRLERLTHS---ISSGKRLSPQHWDFYADL 148
 QY 53 EPIIMELGRGAYGVYKRRHVPSSGOIMAVKIRATVNSQEQRLMDLDSMRTVDCPTV 112
 DB 149 KDLGELGRGAYGVYKRRHVPSSGOIMAVKIRATVNSQEQRLMDLDSMRTVDCPTV 208

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sequence_revision 10-Feb-1996 #text_change 18-Jun-1999

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EF; 98-363/Domain: protein kinase

F:106-114/Region: protein kinase ATP-binding motif

Query Match 51.0%; Score 882; DB 2; Length 395;
Best Local Similarity 51.0%; Pred. No. 8.6e-39;
Matches 180; Conservative 60; Mismatches 87; Indels 26; Gaps 9;

QY 1 SOSKGRK-----NGKIPKAEFQPOSSSTP-----PDDLSKACISIG-
DB 33 SSMGKRRKRLKLNFPNPPKSTARRFTNPTTGVONPHIERLRHSISGKRLSPEDH 92
QY 45 FEVYADDELEPIMELGRGAYGVYVKKRHPVSGQIMAVKRIKRVNSQEQKRLMDLDSMR 104
DB 93 WDFPAEDKDKIGELGRGAYGVYVKKRHPVSGQIMAVKRIKRVNSQEQKRLMDLDSMR 152
QY 105 TVDCEFTYFYGALFREGDVMICELMDTSIDKRYK---QVIDKQITPEDILGKIVSI 161
DB 153 SSQCPYIYQFYGALFREGDVMICELMDTSIDKRYK---QVIDKQITPEDILGKIVSI 210
QY 162 VKALEHLHSKLSVIRHDKVPSNVILNALGOVYKCDFGISGYLVDSVAKTIDAGCKRYMAP 221
DB 211 VKALNHL-KKLEIIRHDKVPSNVILNALGOVYKCDFGISGYLVDSVAKTIDAGCKRYMAP 269
QY 222 ERINPELNQGYSVKSDIWSIGITMELALILRPYDSWGTPEQOLKQVEEPPQLP-AD 280
DB 270 ERIDPSNRQGYDVNSDWSIGITMELALILRPYDSWGTPEQOLKQVEEPPQLP-AD 328
QY 281 KFSA--EFVDTFSGCLAKNSKRPYVPELMOHPEFLHESKGTDVASFVKLLI 331
DB 329 ERSSPSPFIFNVLICITKDESKRPYKELKHPFLIMYERIVYVACVCKIL 381

RESULT 8

T1665
hypochemical protein R0365.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T1665
R:Connell, M.
Submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid R0365.
A:Reference number: Z18556
A:Accession: T1665
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-343 <CON>
A:Cross-references: EMBL:U51994; NID:q1255290; PID:q1255295; PIDN:AAA96067.1; GSPDB:GN00
A:Experimental source: strain Bristol N2; clone R0365
C:Genetics:
A:Gene: CESP:R0365.2
A:Map position: X
A:Introns: 5/1: 35/2: 79/3: 207/3: 291/2
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 50.0%; Score 865.5; DB 2; Length 343;
Best Local Similarity 50.8%; Pred. No. 5.3e-38;
Matches 168; Conservative 64; Mismatches 88; Indels 11; Gaps 6;

QY 2 OSKGRKRN-PGLKIPKAEFQPOSSSTPDDLSKACISIGNQN-FEVKADDELEPIMEL 58
DB 2 ERKGRERKLPKMT-----VMPFVPEFTNPTNEDRCILKLTNESEIEIATDLVLEEL 56
QY 59 GRGAYGVYVKKRHPVSGQIMAVKRIKRVNSQEQKRLMDLDSMRVYDCEFTYFYGAL 118
DB 57 GRGAYGVYVKKRHPVSGQIMAVKRIKRVNSQEQKRLMDLDSMRVYDCEFTYFYGAL 116
QY 119 FRGCDVWICELMDTSIDKRYKQVIDKQITPEDILGKIVSIKALEHLHSKLSVIRH 178
DB 117 FRGCDVWICELMDTSIDKRYKQVIDKQITPEDILGKIVSIKALEHLHSKLSVIRH 176
QY 179 VKRSNVILNALGOVYKCDFGISGYLVDSVAKTIDAGCKRYMAPERINPELNQGYSVKSD 238
DB 177 VKRSNVILNALGOVYKCDFGISGYLVDSVAKTIDAGCKRYMAPERINPELNQGYSVKSD 235

QY 239 IMSLGTMTLALILRPYDSWGTPEQOLKQVEEPPQLPADK-FSAEFYDFTSCKLKN 297
DB 236 VMSLGTITLIEANGTAPRANMKRPPEQLKQVEEPPQLPADK-FSAEFYDFTSCKLKN 295
QY 298 SKERPYPPELMOHPEF-TLHESKGTDVASFV 327
DB 296 YNERPKYPPELMOHPEF-TLHESKGTDVASFV 326

RESULT 9

S71633
MAP kinase kinase (EC 2.7.1.-) SAPK3 isoform B - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71633
R:Quenda, A.; Alonso, G.; Morrice, N.; Jones, M.; Meier, R.; Cohen, P.; Nebreda, A.R.
EMBO J 15, 4156-4164, 1996
A:Title: Purification and cDNA cloning of SAPK3, the major activator of Rb/p38 in s
A:Reference number: S71631; MUID:97015116; PMID:8861944
A:Accession: S71633
A:Molecule type: mRNA
A:Residues: 1-162 <CUE>
A:Cross-references: EMBL:X98067; NID:q1495709; PIDN:CAA66670.1; PID:q1495710
A:Experimental source: cell type fibroblast
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1996
C:Genetics:
A:Gene: SAPK3b
C:Superfamily: kinase-related transforming protein; protein kinase homology
F:1-162/Domain: protein kinase homology (fragment) <KIN>

Query Match 47.5%; Score 822; DB 2; Length 162;
Best Local Similarity 98.1%; Pred. No. 4.6e-36;
Matches 159; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 69 MRHVPSCQIMAVKRIKRVNSQEQKRLMDLDSMRVYDCEFTYFYGALFREGDVMIC 128
DB 1 MRHVPSCQIMAVKRIKRVNSQEQKRLMDLDSMRVYDCEFTYFYGALFREGDVMIC 60
QY 129 ELMDTSIDKRYKQVIDKQITPEDILGKIVSIKALEHLHSKLSVIRHDKVPSNVILNA 188
DB 61 ELMDTSIDKRYKQVIDKQITPEDILGKIVSIKALEHLHSKLSVIRHDKVPSNVILNA 120
QY 189 LGQYKMDCFGISGYLVDSVAKTIDAGCKRYMAPERINPELNQ 230
DB 121 LGQYKMDCFGISGYLVDSVAKTIDAGCKRYMAPERINPELNQ 162

RESULT 10

T22107
hypochemical protein F42G10.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22107; T26026
R:Harris, B.
Submitted to the EMBL Data Library, February 1995

A:Reference number: Z19515
A:Accession: T22107
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-363 <MID>
A:Cross-references: EMBL:Z48230; PIDN:CAA88264.1; GSPDB:GN00028; CESP:F42G10.2
A:Experimental source: clone F42G10
R:Lennard, N.
Submitted to the EMBL Data Library, May 1997
A:Reference number: Z20139
A:Accession: T26026
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-363 <MID>
A:Cross-references: EMBL:Z95122; PIDN:CAB08355.1; GSPDB:GN00028; CESP:F42G10.2
A:Experimental source: clone VZC374L

C:Genetics:

A:Gene: CESP:F42G10.2

A:Map position: X

A:Introns: 42/2; 95/3; 136/3; 176/3; 236/3; 259/3; 281/3; 310/2; 332/2

C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match

Best Local Similarity 36.3%; Score 628.5; DB 2; Length 363;

Matches 136; Conservative 56; Mismatches 111; Indels 39; Gaps 7;

QY 21 QPQSSSTPRDLSDKACISIGNON-----FEVAKADLEPIIM 56
 DB 16 PPSLSTRPSLSVN-----GNEKLPEESVLRSLSTGLKYPDDEHLITFSSANLQDQ 70
 QY 57 ELGRGAGVVEKMRHVPSSQIMAVKRIKRA-TYNSQOKRLMDLDSMRVTCPTVTF 115
 DB 71 AIGNGNGTYKMKHKEGKLIAYKRIKCNNGHGEQIRLREHDTYKSEKGPIMVRY 130
 QY 116 GALEFREGDVMICMELMDTSLDKFYKOV-IDKQGITPEDILGKIAVYKALEHLSKLSV 174
 DB 131 GAIFSEGDVMICMELMDISMDLTLYKRVYMKNSRLNENYGHITCTVDALDYLKEKLI 190
 QY 175 IHHDVKSNTVLINAGVKKMDDEGISGLVDSVAKTIDAGCKPTAPRINELNOKYS 234
 DB 191 IHHDVKSNTVLINAGVKKMDDEGISGLVDSVAKTIDAGCKPTAPRINELNOKYS 247
 QY 235 VKSDIMSLGITMELALIRPPYDSMGTPFOOLKOVVEEPSQOLPADK---FSAFVDF 290
 DB 248 VRSDVMSLGITLVEIATNGKFPYQEMNSLFQDIATVSSDPRILHDSIDFHYSLPLVFI 307
 QY 291 SOCLTKKSKRPYTPPELMQHPFTLHESKGTDVASFVKLLIG 332
 DB 308 NCLTKDRHRPRKYDTLKSFPDYRIYAVAGPEIEE-AKRILG 348

RESULT 11

T26025

hypothetical protein VZC374L.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T26025

R:Lenard, N.

submitted to the EMBL Data Library, May 1997

A:Reference number: Z20139

A:Accession: T26025

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-359 <WILD>

A:Cross-references: EMBL:Z59122; PIDD:CA08354.1; GSPDB:GN00028; CESP:VZC374L.1

A:Experimental source: clone VZC374L

C:Genetics:

A:Gene: CESP:VZC374L.1

A:Map position: X

A:Introns: 40/2; 93/3; 132/3; 172/3; 232/3; 255/3; 277/3; 306/2; 328/2

C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match

Best Local Similarity 45.6%; Score 618; DB 2; Length 359;

Matches 131; Conservative 47; Mismatches 99; Indels 10; Gaps 5;

QY 51 DLEPIMELRGAGVVEKMRHVPSSQIMAVKRIKRA-TYNSQOKRLMDLDSMRVTCPT 110
 DB 63 NLRHLISQVAGYGVVHKMHQNHESGLIAVKRIKRY-NICDQTRLKEHDTYKSEKVP 121
 QY 111 TYTFGALFREGDVMICMELMDTSLDKFYKOV-IDKQGITPEDILGKIAVYKALEHLS 169
 DB 122 IVKFGAGFSEGDVMICMELMDISMDLTLYKRVYMKNSRLNENYGHITCTVDALDY 181
 QY 170 SKLSYIHHDVKSNTVLINAGVKKMDDEGISGLVDSVAKTIDAGCKPTAPRINELN 229
 DB 182 RKLNIHHDVKSNTVLINAGVKKMDDEGISGLVDSVAKTIDAGCKPTAPRINELN 238
 QY 230 QKGSVKSVDIMSLGITMELALIRPPYDSMGTPFOOLKOVVEEPSQOLPADKSAFV 288

DB 239 MDXYDIRSDVMSLGITLVEIATNGKFPYQEMNSLFQDIATVSSDPRILHDSIDF 298
 QY 289 ---FTSOLKRSKRPYTPPELMQHPFTLHESKGTDVASFVKLLIG 332
 DB 299 LCRFINLCLRNKKNDKRRKYVNLKTFSEKMYAVGPDIEE-AKRILG 344

RESULT 12

T16583

hypothetical protein K08A8.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16583

R:Pauley, A.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid K08A8.

A:Reference number: Z18541

A:Accession: T16583

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-505 <PAU>

A:Cross-references: EMBL:U08377; NID:G1022968; PID:G1022969; PIDD:AAA79746.1; CESP

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:K08A8.1

A:Introns: 62/1; 139/3; 187/3; 291/3; 345/2; 380/2; 448/3

Query Match

Best Local Similarity 35.3%; Score 610.5; DB 2; Length 505;

Matches 131; Conservative 63; Mismatches 116; Indels 21; Gaps 7;

QY 13 KIPKEAFEPQISSTPRDLSDKACISIGNON-----EVKAD-DLEPIMELRGGA 62
 DB 26 QMPQAPRHPHPSRS---NDHNVKMLKQAEENGUYLTQGNRRKADKEIQFVEDIGHGS 82
 QY 63 YGVVEKMRHVPSSQIMAVKRIKRA-TYNSQOKRLMDLDSMRVTCPTVTFYALREG 122
 DB 83 CGTYVKRY--KSVIMAVTMTPTSNSYSESRILMDLVCISFDCTYVRCFYFTNF 140
 QY 123 DWIMCELMDSLDKFKYKOVIDKQGITPEDILGKIAVYKALEHLSKLSVIRVYKPS 182
 DB 141 DVAVCECMATCIDRL---LIRIKQPIPERIEIKLSITIKALHYLTKHQIHNDVYKPS 197
 QY 183 NYLINAGVKKMDDEGISGLVDSVAKTIDAGCKPTAPRINELNOKYSVKSIDTSL 242
 DB 198 NILLDMSGVYKICLDFEIGARLIESRAHSKQAGCPLYMGPERIDPN-NFDSYDIRSDVMS 256
 QY 243 GITMELALIRPPYDSMGTPFOOLKOVVEEPSQOLPADKSAFVDFTSOLKRSKRP 302
 DB 257 GVTLEIATNGKFPY--GTFEDMSKILLNDEPRIDPAKFSDFCOLVESCLDRDPTMR 314
 QY 303 TYPPELMQHPFTLHESKGTDVASFVKLLIGD 333
 DB 315 NYDMLLOHPFVNVHKEIETDVEWEPADVMD 345

RESULT 13

S18648

Protein kinase w1sl (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 22-Nov-1993 #sequence_revision 10-Feb-1995 #text_change 10-Dec-1999

C:Accession: S18648; T40435

R:Marbrick, E.; Panties, P.A.

EMBO J. 10, 4291-4299, 1991

A:Title: The w1sl protein kinase is a dosage-dependent regulator of mitosis in schi-

A:Reference number: S18648; MUID:92097549; PMID:1756736

A:Accession: S18648

A:Molecule type: DNA

A:Residues: 1-605 <MAR>

A:Cross-references: EMBL:X62631; NID:G5141; PIDD:CAA44499.1; PID:G5142

R:Lyne, M.H.; Rajendram, M.A.; Barrett, B.G.; Chillingworth, T.; Churcher, C.M.

submitted to the EMBL Data Library, August 1999

R;Zheng, C.F.; Guan, K.L.
J. Biol. Chem. 268, 11435-11439, 1993
A:Title: Cloning and characterization of two distinct human extracellular signal-regulated
A:Reference number: A46723; MUID:93266604; PMID:8388392
A:Accession: B46723
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-295, 'g', 296-393 <ZHE>
A:Cross-references: GB:L11284; NID:9307183
A:Note: sequence extracted from NCBI backbone (NCBI:132852)
R:Mansour, S.J.; Resing, K.A.; Candi, J.M.; Hermann, A.S.; Gloer, J.W.; Herskind, K.R.;
J. Biochem. 116, 304-314, 1994
A:Title: Mitogen-activated protein (MAP) kinase phosphorylation of MAP kinase kinase: De
A:Reference number: JC2504; MUID:95122457; PMID:7822248
A:Accession: JC2504
A:Molecule type: protein
A:Residues: 5-96, 98-349, 354-393 <MAN>
A:Note: phosphorylation sites determined in vitro
C:Comment: This enzyme is activated by protein kinase raf-1 (see PIR:A00637). It in turn
C:Genetics:
A:Gene: GDB:PRKML; MEK1; MAPKK1
A:Cross-references: GDB:136418; OMIM:176872
C:Complex: monomer
C:Function:
A:Description: catalyzes the formation of specific peptidyl-l-threonine-phosphate and pept
A:Pathway: MAP kinase cascade
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: alternative splicing; ATP; monomer; phosphoprotein; phosphotransferase; ser1
F:1-393/Product: MAP kinase kinase 1, splice form A #status experimental <MATA>
F:1-146, 173-393/Product: MAP kinase kinase 1, splice form B #status predicted <MATB>
F:66-361/Domain: protein kinase homology <KIN>
F:74-82/Region: protein kinase ATP-binding motif
F:97, 114, 190, 192/Active site: Lys, Glu, Asp, Lys #status predicted
F:218, 222/Binding site: phosphate (Ser) (covalent) (by raf-1 kinase) #status predicted
F:292, 386/Binding site: phosphate (Thr) (covalent) (by raf-1 kinase) #status experimental

Query Match 33.9%; Score 587; DB 1; Length 393;
Best Local Similarity 38.0%; Pred. No. 1, 3e-23;
Matches 125; Conservative 62; Mismatches 90; Indels 52; Gaps 7;

QY 46 EVKADLEPIMELGAGYGVEMKRVPSGQIMAVKRIATVNSQEQRLMDLDSMRT 105
DB 62 ELKDDDFEKISLGLAGNGGVFRKSHKPSGLVMARKLIHLKPAIRMQIIRELOV-LHE 120
QY 106 VDCPTVTFTYGFALFREGDVMICMLMD-TSLDKFYQVVIDKGQTIPEIDIGKIAVSIVKA 164
DB 121 CNSPIYGVFYGAFFYSDGEISICMEHMDGSLD---QVLKAGRIPEQIIIGKYSIAVIKG 176
QY 165 LEHLHSKLSVIRHDKYKPSNVNLINALGVKMCDEGISGYLVDSVAKTIDAGCKPYMAPERI 224
DB 177 LTVLEKHKIMHRDVKPSNIIIVNSRGEIKLCDFGVSGQLIDSMANSF-VGTRSYMSPER- 234
QY 225 NPELNOKGYSVKSDIMSLGITMIELAILRFPY-----DSWGTG----- 262
DB 235 ---LQGTIVSYQSDIWSMGLSLVENAVGRYPIPPDAKLELMFGCQVEGDAETPPRPR 291
QY 263 -----FQQLKQVVEPPSPQLPADKPSAEFVFTSCLKNSKERPT 303
DB 292 TPGRPILSSYGMDSRPMAIFELLDYIVNEPPKPLPSGVSTLEQDFVNNCKLIKPNAPRAD 351
QY 304 YPELMOHPFTLHESKGTDVASFVKLIIG 332
DB 352 LKQLMVAHAFIKRSDAEVDFAGWLCSTIG 380

Search completed: June 6, 2003, 09:11:51
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 09:04:09 ; Search time 11 seconds
(without alignments)
1255.602 Million cell updates/sec

Title: US-09-593-288-2
Perfect score: 1731
Sequence: 1 SOSKGRKRNPKLIPKEAFE.....TLHESKGTDAVFAFKLILGD 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1731	100.0	334	1	MPK6_HUMAN
2	1705	98.5	334	1	MPK6_MOUSE
3	1367	79.0	318	1	MPK3_HUMAN
4	1334	77.1	314	1	MPK3_MOUSE
5	924.5	53.4	446	1	MPK2_XENLA
6	920	53.1	397	1	MPK4_MOUSE
7	919	53.1	399	1	MPK4_HUMAN
8	697	40.3	419	1	MPK7_HUMAN
9	696	40.2	487	1	HEP DROME
10	628.5	36.3	363	1	YR6Z_CAEEL
11	607.5	35.1	605	1	WIS1_SCHPO
12	606	35.0	668	1	PBS2_YEAST
13	587.5	33.9	448	1	MPK5_YEAST
14	587	33.9	392	1	MPK1_HUMAN
15	587	33.9	392	1	MPK1_MOUSE
16	587	33.9	392	1	MPK1_RAT
17	586.5	33.9	401	1	MPK2_MOUSE
18	586	33.9	392	1	MPK1_MOUSE
19	584	33.7	388	1	MPK1_RABIT
20	583	33.7	400	1	MPK1_SERCA
21	575	33.2	394	1	MPK1_XENLA
22	572	33.0	393	1	MPK1_CRIGR
23	571	33.0	398	1	MPK2_MOUSE
24	565	32.6	397	1	MPK2_MOUSE
25	563	32.5	400	1	MPK2_MOUSE
26	553	31.9	438	1	MPK5_HUMAN
27	541	31.3	433	1	DSOR_DROME
28	525	30.3	387	1	MEK2_CAEEL
29	490.5	28.3	435	1	FU27_USTMA
30	481	27.8	515	1	STF7_YEAST
31	478.5	27.6	363	1	SKH1_SCHPO
32	476.5	27.5	508	1	MKR1_YEAST
33	456.5	26.4	340	1	BYR1_SCHPO

34	448.5	25.9	506	1	MPK2_YEAST	P32491 saccharomyc
35	418.5	24.2	491	1	STK3_HUMAN	Q13188 homo sapien
36	418	24.1	487	1	STK4_HUMAN	Q13043 homo sapien
37	368.5	21.3	968	1	ST10_MOUSE	Q94804 homo sapien
38	364.5	21.1	966	1	ST10_MOUSE	Q55098 mus musculu
39	350	20.2	589	1	STF7_CANAL	P46599 candida alb
40	335	19.4	426	1	ST25_HUMAN	Q00506 homo sapien
41	332.5	19.2	443	1	ST24_HUMAN	Q97460 homo sapien
42	330	19.1	426	1	ST25_MOUSE	Q92241 mus musculu
43	316.5	18.3	658	1	PAK1_SCHPO	P50527 schizosacch
44	315	18.2	544	1	PAK3_RAT	Q62829 rattus norv
45	312.5	18.1	393	1	NTF4_TORAC	Q40532 nicotiana t

ALIGNMENTS

RESULT 1	ID	MPK6_HUMAN	STANDARD;	PRT;	334 AA.
AC	P52564;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Dual specificity mitogen-activated protein kinase 6				
DE	(EC 2.7.1.-) (MAP kinase kinase 6) (MAPK 6) (MAPK/ERK kinase 6)				
DE	(SAPK3).				
GN	MAP2K6 OR PRKMK6 OR MKK6 OR MEK6.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND MUTAGENESIS.				
RC	TISSUE=Skeletal muscle;				
RX	MEDLINE=96182129; PubMed=8622669;				
RA	Raingeaud J., Whitmarsh A.J., Barrett T., Derrijard B., Davis R.J.;				
RT	"MKK3- and MKK6-regulated gene expression is mediated by the p38				
RT	mitogen-activated protein kinase signal transduction pathway.";				
RL	Mol. Cell. Biol. 16:1247-1255(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=T-cell;				
RX	MEDLINE=96212215; PubMed=8626699;				
RA	Stein B., Brady H., Yang M.X., Young D.B., Barbosa M.S.;				
RT	"Cloning and characterization of MEK6, a novel member of the mitogen-				
RT	activated protein kinase cascade.";				
RL	J. Biol. Chem. 271:11427-11433(1996).				
RN	[3]				
RP	SEQUENCE FROM N.A., AND MUTAGENESIS (SHORT FORM).				
RC	TISSUE=Placenta;				
RX	MEDLINE=96216153; PubMed=8621675;				
RA	Han J., Lee J.-D., Jiang Y., Li Z., Feng L., Ulevitch R.J.;				
RT	"Characterization of the structure and function of a novel MAP kinase				
RT	kinase (MKK6).";				
RL	J. Biol. Chem. 271:2886-2891(1996).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96278799; PubMed=8663074;				
RA	Woriguchi T., Kuroyanagi N., Yamaguchi K., Gotoh Y., Irie K., Kano T.,				
RA	Shirakabe K., Muro Y., Shibuya H., Matsumoto K., Nishida E.,				
RA	Hagiwara M.;				
RT	"A novel kinase cascade mediated by mitogen-activated protein kinase				
RT	kinase 6 and MKK3.";				
RL	J. Biol. Chem. 271:13675-13679(1996).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97015116; PubMed=8861944;				
RA	Cebenda A., Alonso G., Morrice N., Jones M., Meier R., Cohen P.,				
RA	Nebreda A.R.;				
RT	"Purification and cDNA cloning of SAPK3, the major activator of				
RT	RK/p38 in stress- and cytokine-stimulated monocytes and epithelial				
RT	cells.";				

EMBO J. 15:4156-4164(1996).

[6]

RA CLEAVAGE BY ANTHRAX LETHAL FACTOR.
MEDLINE-20558083; PubMed-11104681;
Vitalie G., Bernardi L., Napolitano G., Mock M., Montecucco C.;
RT "Susceptibility of mitogen-activated protein kinase family
members to proteolysis by anthrax lethal factor."
RL Biochem. J. 352:739-745(2000).

CC -1- FUNCTION: CATALYZES THE CONCOMITANT PHOSPHORYLATION OF A THREONINE
AND A TYROSINE RESIDUE IN MAP KINASE P38 EXCLUSIVELY.
CC -1- ENZYME REGULATION: PROBABLY ACTIVATED BY DUAL PHOSPHORYLATION ON
SER-207 AND THR-211.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: MKK6 AND MKK6B (SHOWN HERE); ARE
PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: MKK6 IS ONLY EXPRESSED IN SKELETAL MUSCLE.
CC MKK6B, ON THE OTHER HAND, IS FOUND IN SKELETAL MUSCLE, HEART, AND
IN LESSEER EXTENT IN LIVER OR PANCREAS.
CC -1- INDUCTION: STRONGLY ACTIVATED BY UV, ANISOMYCIN, AND OSMOTIC SHOCK
BUT NOT BY PHORBOL ESTERS, NGF OR EGF.
CC -1- PTR: VERY LOW AUTOPHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.

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or send an email to license@isb-sib.ch).

DR EMBL: U39657; AAC50389.1; -
DR EMBL: U39656; AAC50388.1; -
DR EMBL: U49732; AAB05035.1; -
DR EMBL: U39065; AAB03705.1; -
DR EMBL: U39064; AAB03708.1; -
DR EMBL: D87905; BAA13496.1; -
DR EMBL: X96757; CAA65532.1; -
DR Genew: HGN:6846; MAP2K6.
DR MIM: 601254; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF000069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase; Tyrosine-protein kinase;
KW ATP-binding; Phosphorylation; Alternative splicing.
FT DOMAIN 53 314 PROTEIN KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 BY SIMILARITY.
FT ACT_SITE 179 179 PHOSPHORYLATION (PROBABLE).
FT MOD_RES 207 207 PHOSPHORYLATION (PROBABLE).
FT MOD_RES 211 211 CLEAVAGE (BY ANTHRAX LETHAL FACTOR).
FT SITE 14 15 MISSING (IN ISOFORM MKK6).
FT VARSLIC 1 56 S->E: CONSTITUTIVE ACTIVATION ACCORDING
TO REF. 1 BUT NOT TO REF. 3.
FT MUTAGEN 207 207 S->A: INACTIVATION.
FT MUTAGEN 211 211 T->E: CONSTITUTIVE ACTIVATION ACCORDING
TO REF. 1 BUT NOT TO REF. 3.
FT MUTAGEN 211 211 T->A: INACTIVATION.
FT CONFLICT 125 125 V->M (IN REF. 3).
FT SEQUENCE 334 AA; 37492 MW; 4ECA801522216AF CMC64;

Query Match 100.0%; Score 1731; DB 1; Length 334;
Best Local Similarity 100.0%; Pred. No. 2, 2e-117;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SOSGKKRNPGLKIPKAEFQPTSSPPRLDSKACISIGNONFEVAKADLEPIMLGR 60
|||||

Db 2 SOSGKKRNPGLKIPKAEFQPTSSPPRLDSKACISIGNONFEVAKADLEPIMLGR 61

QY 61 GATGVYKRRHVSQGMVAVKRRATVNSQGRRLMDLDISMTVDCPFTVYGAFLR 120
|||||

Db 62 GATGVYKRRHVSQGMVAVKRRATVNSQGRRLMDLDISMTVDCPFTVYGAFLR 121

QY 121 EGDWVICMELMDTSLDKFYQVYDKQOTIPEDILGKTAIVSKALVHLHSLVYHNDVK 180
|||||

Db 122 EGDWVICMELMDTSLDKFYQVYDKQOTIPEDILGKTAIVSKALVHLHSLVYHNDVK 181

QY 181 PSVVLINAGGVKMCDCGIGYLVDSVAKTIDAGCKRPMAPERINPELNQKGYSVKSDIW 240
|||||

Db 182 PSVVLINAGGVKMCDCGIGYLVDSVAKTIDAGCKRPMAPERINPELNQKGYSVKSDIW 241

QY 241 SLGITMELIALILRPYDSWGTPEQOLKQVVEEPPQADPKFSAEVDFTSQCLKNKE 300
|||||

Db 242 SLGITMELIALILRPYDSWGTPEQOLKQVVEEPPQADPKFSAEVDFTSQCLKNKE 301

QY 301 RPTYPELMQHPFTLHESKGTVDVAFVLLIGD 333
|||||

Db 302 RPTYPELMQHPFTLHESKGTVDVAFVLLIGD 334

RESULT 2

MPK6_MOUSE STANDARD; PTR: 334 AA.

ID MPK6_MOUSE

AC P70236;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Dual specificity mitogen-activated protein kinase 6 (MAPK 6) (MAPK/ERK kinase 6) (EC 2.7.1.1) (MAP kinase kinase 6) (MAPK 6) (MAPK/ERK kinase 6)

DE (SAPK3)

GN MAP2K6 OR PRPK6 OR SAPK3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclauognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-97015116; PubMed-8861944;

RA Cuenda A., Alonso G., Morrice N., Jones M., Meier R., Cohen P., Nebreda A.R.

RT "Purification and cDNA cloning of SAPK3, the major activator of Rk/p38 in stress- and cytokine-stimulated monocytes and epithelial cells."

RT EMBL J. 15:4156-4164(1996).

CC -1- FUNCTION: CATALYZES THE CONCOMITANT PHOSPHORYLATION OF A THREONINE AND A TYROSINE RESIDUE IN MAP KINASE P38 EXCLUSIVELY.

CC -1- ENZYME REGULATION: PROBABLY ACTIVATED BY DUAL PHOSPHORYLATION ON SER-207 AND THR-211 (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MAP KINASE KINASE SUBFAMILY.

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DR EMBL: X97052; CAA65764.1; -
DR MGD: MGI:1346870; Map2K6.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF000069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase; Tyrosine-protein kinase;

KW ATP-binding; Phosphorylation. PROTEIN KINASE.
 FT DOMAIN 53 314
 FT NP_BIND 59 67
 FT BINDING 82 82
 FT ACT_SITE 179 179
 FT MOD_RES 207 207
 FT MOD_RES 211 211
 SQ SEQUENCE 334 AA: 37432 MW: 62CEFC28AF50BAC CRC64;

Query Match 98.5%; Score 1705; DB 1; Length 334;
 Best Local Similarity 97.9%; Pred. No. 1,6e-115;
 Matches 326; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 SOSGKRRNPGLIKIKFAEPQSTPRDDSKACISIGNONFEVKADDELPIMELGR 60
 DB 2 SOSGKRRNPGLIKIKFAEPQSTPRDDSKACISIGNONFEVKADDELPIMELGR 61
 QY 61 GAYGVKRRHVPSCQIMAVKRIRATVNSQEQRLMDLDSMRVDCFTVYFALFR 120
 DB 62 GAYGVKRRHVPSCQIMAVKRIRATVNSQEQRLMDLDSMRVDCFTVYFALFR 121
 QY 121 EGDVWICMELMDTSLDKFYKQYIDGQTPEDILGKINAIYKALEHLSKLSVHRDYK 180
 DB 122 EGDVWICMELMDTSLDKFYKQYIDGQTPEDILGKINAIYKALEHLSKLSVHRDYK 181
 QY 181 PSNVLINALGOVKMCDGFSIGYLVDSVAKTIDAGCKPYMAPRINPELNOKGYSKSDIM 240
 DB 182 PSNVLINALGOVKMCDGFSIGYLVDSVAKTIDAGCKPYMAPRINPELNOKGYSKSDIM 241
 QY 241 SLGTTMELATLRPPYDSWGTTPFOOLKOVVEPSQOLPADKFSAEFVDTSOCLKNKSE 300
 DB 242 SLGTTMELATLRPPYDSWGTTPFOOLKOVVEPSQOLPADKFSAEFVDTSOCLKNKSE 301
 QY 301 RPTYPELMQHPFFTLHESKGTIVASFWKLIIGD 333
 DB 302 RPTYPELMQHPFFTLHESKADVASFWKLIIGD 334

RESULT 3
 ID MPK3_HUMAN STANDARD; PRT; 318 AA.
 AC P46734;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dual specificity mitogen-activated protein kinase kinase 3
 DE (EC 2.7.1.1) (MAP kinase kinase 3) (MAPKK 3) (MAPK/ERR kinase 3).
 GN MAP2K3 OR PRKMK3 OR MKK3 OR MEK3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=95141073; Pubmed=7839144;
 RA Derjard B., Raligeaud J., Barrett T., Wu I.-H., Han J.,
 RA Ulevitch R.J., Davis R.J.;
 RT "Independent human MAP-kinase signal transduction pathways defined by
 RT MEK and MKK isoforms.";
 RL Science 267:682-685(1995).
 RN [2]
 RP MUTAGENESIS.
 RA MEDLINE=96182129; Pubmed=8622669;
 RA Raligeaud J., Whitmarsh A.J., Barrett T., Derjard B., Davis R.J.;
 RT "MKK3- and MKK6-regulated gene expression is mediated by the p38
 RT Mol. Cell. Biol. 16:1247-1255(1996).
 CC -1- FUNCTION: DUAL SPECIFICITY KINASE. IS ACTIVATED BY CYTOKINES AND
 CC ENVIRONMENTAL STRESS IN VIVO. CATALYZES THE CONCOMITANT
 CC PHOSPHORYLATION OF A THREONINE AND A TYROSINE RESIDUE IN THE MAP
 CC KINASE P38.
 CC -1- ENZYME REGULATION: ACTIVATED BY DUAL PHOSPHORYLATION ON SER-189

CC AND THR-193.
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IS SEEN IN THE SKELETAL
 CC MUSCLE. IT IS ALSO WIDELY EXPRESSED IN OTHER TISSUES.
 CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: L36719; AAC41718.1;
 CC Genbank: HGNC:6843; MAP2K3.
 CC MIM: 602315;
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR002290; Ser_thr_pkinase.
 CC Pfam: PF00069; Pkinase; 1.
 CC ProDom: PD000001; Euk_Pkinase; 1.
 CC SMART: SM00220; S_TKc; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC DR TRANSFERASE; Serine/threonine-protein kinase; Tyrosine-protein kinase;
 CC KW ATP-binding; Phosphorylation.
 CC FT DOMAIN 35 296
 CC FT NP_BIND 41 49
 CC FT BINDING 64 64
 CC FT ACT_SITE 161 161
 CC FT MOD_RES 189 189
 CC FT MOD_RES 193 193
 CC FT MOD_RES 189 189
 CC FT MOTAGEN 193 193
 CC FT MOTAGEN 193 193
 CC FT MOTAGEN 193 193
 CC SQ SEQUENCE 318 AA: 36172 MW: 966821BE4B6E0DA CRC64;

Query Match 79.0%; Score 1367; DB 1; Length 318;
 Best Local Similarity 82.7%; Pred. No. 2.8e-91;
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;

QY 22 PQTSSTPRDDSKACISIGNONFEVKADDELPIMELGRGAYGVKRRHVPSCQIMAVK 81
 DB 5 PAVNPPRRNLDSRTFTIGDRNFEVADDLVTISELGRGAYGVKRRHVPSCQIMAVK 64
 QY 82 RIRATVNSQEQRLMDLDSMRVDCFTVYFALFRSGDWICMELMDTSLDKFYRK 141
 DB 65 RIRATVNSQEQRLMDLDSMRVDCFTVYFALFRSGDWICMELMDTSLDKFYRK 124
 QY 142 VIDKGTIPEDILGKINAIYKALEHLSKLSVHRDYKPSNVLINALGOVKMCDGFSIG 201
 DB 125 VLDKMTIPEDILGKINAIYKALEHLSKLSVHRDYKPSNVLINALGOVKMCDGFSIG 184
 QY 202 YLVDSVAKTIDAGCKPYMAPRINPELNOKGYSKSDIMSLGITMELATLRPPYDSWGT 261
 DB 165 YLVDSVAKTIDAGCKPYMAPRINPELNOKGYSKSDIMSLGITMELATLRPPYDSWGT 244
 QY 262 PFOOLKOVVEPSQOLPADKFSAEFVDTSOCLKNKSEKPTYPELMQHPFFTLHESKGT 321
 DB 245 PFOOLKOVVEPSQOLPADKFSAEFVDTSOCLKNKSEKPTYPELMQHPFFTLHESKGT 304
 QY 332 DVASFWKLIIGD 333
 DB 305 DIAAFVKKILGE 316

RESULT 4
 ID MPK3_MOUSE STANDARD; PRT; 314 AA.
 AC O09110;

FT DOMAIN 22 40 SER-RICH.
 FT DOMAIN 149 414 PROTEIN KINASE.
 FT NP_BIND 155 163 ATP (BY SIMILARITY).
 FT BINDING 178 178 ATP (BY SIMILARITY).
 FT ACT_SITE 276 276 BY SIMILARITY.
 FT MOD_RES 304 304 PHOSPHORYLATION (BY RAF) (BY SIMILARITY).
 FT MOD_RES 308 308 PHOSPHORYLATION (BY RAF) (BY SIMILARITY).
 FT VARSPIC 51 51 G->GLIINCDNMQS (IN ISOFORM 2).
 FT MOTAGEN 178 178 K->R: LOSS OF ACTIVITY.
 SQ SEQUENCE 446 AA; 50100 MW; 96B5DCA0695662 CRC64.

Query Match 53.4%; Score 924.5; DB 1; Length 446;
 Best Local Similarity 53.4%; Pred. No. 2.4e-59;
 Matches 183; Conservative 51; Mismatches 92; Indels 17; Gaps 5;

QY 1 SOSKGGKRRNPGLK-----IPKFAFOPOTSSPPRNDLSKACISIG-NONEFKADL 52
 DB 95 SYGKODLRISGAAALSTNEQATKRLRLRHS-----IESGKLIKISPEQHWDFTAIDL 149
 QY 53 EPIWELGRCAYGVYKRRHVPSSQIMAVKRIRATVNSQEQRLMDIDISMRVDCPPTV 112
 DB 150 KDLGEIGRGAYGVYKRRHVPSSQIMAVKRIRATVNSQEQRLMDIDLVVRRSDCPYIV 209
 QY 113 TFYGALEFREDGVCWICMELMTSDIKFKYKVID-KGOTIPEDILKIAVSIKALEHHSK 171
 DB 210 QFYGALFREDGVCWICMELMTSDIKFKYKVID-KGOTIPEDILKIAVSIKALEHHSK 269
 QY 172 LSVIHRDVPKSNVNLINALGVKMGDFGSGYVDSVAKTIDAGCKPYMAPERINDELINOK 231
 DB 270 LKIHIDIKPSNILLDTNGNIKLCDFGSGYVDSVAKTIDAGCKPYMAPERIDPSASRQ 329
 QY 232 GYSKSDISLGTITMELALIRPPYDSWGPFOQLKOVVEEPSPOLPAD--KFSAEFVD 288
 DB 330 GYDVRSDVSLGTITLALIRPPYDSWGPFOQLKOVVEEPSPOLPAD--KFSAEFVD 389
 QY 289 FTSOCLKNSKERPTYPELMOPHFFTLHESKGTDVASFYVLL 331
 DB 390 FYNQCLTKDESKRPRKYLKHPFLIMTEERTVDVAGYVKIL 432

RESULT 6
 MPK4_MOUSE STANDARD; PRT; 397 AA.

AC P47809;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dual specificity mitogen-activated protein kinase kinase 4
 DE (EC 2.7.1.-) (MAP kinase kinase 4) (MAPK 4) (MAPK/ERK kinase 4) (JNK activating kinase 1) (C-JUN N-terminal kinase kinase 1) (JNK kinase 1)
 DE (JUNK 1) (SAPK/ERK kinase 1) (SEK1)
 GN MAP2K4 OR PRKMK4 OR JUNK1 OR SEK1 OR SEK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=95089821, PubMed=7997269;
 RA Sanchez I., Hughes R.T., Mayer B.J., Yee K., Woodgett J.R., Avruch J., Kyriakis J.M., Zon L.I.;
 RT "Role of SAPK/ERK kinase-1 in the stress-activated pathway regulating transcription factor c-Jun.";
 RL Nature 372:794-798(1994).
 RP REVISIONS.
 RA Zon L.I.;
 RL Submitted (DEC-1996) to the EMBL/Genbank/DBD databases.
 CC -1- FUNCTION: DUAL SPECIFICITY KINASE THAT ACTIVATES THE JUN KINASES MAPK8 (JNK1) AND MAPK9 (JNK2) AS WELL AS MAPK14 (P38) BUT NOT MAPK1 (ERK2) OR MAPK3 (ERK1).
 CC -1- TISSUE SPECIFICITY: IS EXPRESSED ABUNDANTLY IN THE ADULT

CC BRAIN AND MUSCLE.
 CC -1- P-TM: ACTIVATED BY PHOSPHORYLATION ON SER/THR BY MAP KINASE KINASE KINASES (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.

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CC EMBL: U18310; AAB81554.1; -
 CC MGI: 1346869; Map2k4.
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR002290; Ser_thr_pkinase.
 CC Pfam: PF00069; pkinase.1.
 CC Prodom: PD000001; Euk_pkinase.1.
 CC SMART: SM00220; S_TKc.1.
 CC PROSITE: PS00107; PROTEIN_KINASE_AAP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferase: Serine/threonine-protein kinase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
 CC DOMAIN 5 17 GLY/SER-RICH.
 CC FT 100 366 PROTEIN KINASE.
 CC FT NP_BIND 103 111 ATP (BY SIMILARITY).
 CC FT BINDING 129 129 ATP (BY SIMILARITY).
 CC FT ACT_SITE 227 227 BY SIMILARITY.
 CC FT MUTAGEN 129 129 K->R: LOSS OF ATP-BINDING ACTIVITY.
 CC FT SEQUENCE 397 AA; 44113 MW; B9C6688184E53D CRC64;

Query Match 53.1%; Score 920; DB 1; Length 397;
 Best Local Similarity 51.6%; Pred. No. 4.4e-59;
 Matches 182; Conservative 57; Mismatches 90; Indels 24; Gaps 6;

QY 1 SOSKGGKRR-----NPGIKRKEAFQQTSTP-----PRDLSKACISIG-NON 44
 DB 33 SMOGKRRKALKINFPANPPKSTAPRTLTNTGVOHPHIERLTHSIESGKLIKISPEQH 92
 QY 45 FEVKADDEPIWELGRCAYGVYKRRHVPSSQIMAVKRIRATVNSQEQRLMDIDISMR 104
 DB 93 WDFTEADLKDLGEIGRGAYGVYKRRHVPSSQIMAVKRIRATVNSQEQRLMDIDLVV 152
 QY 105 TVDGFYTFYGALEFREDGVCWICMELMTSDIKFKYK--QVIDKGOTIPEDILKIAVSI 161
 DB 153 SSDDPYIVQFYGALEFREDGVCWICMELMTSDIKFKYKYSVDL--DVPEILIGKTLAT 210
 QY 162 VKALEHLHSLVSIHRDVPKSNVNLINALGVKMGDFGSGYVDSVAKTIDAGCKRYMAP 221
 DB 211 VKALNHLKENIKIHRDIPKSNILLDRSGNIKLCDFGSGYVDSVAKTIDAGCKRYMAP 270
 QY 222 ERINDELINOKYGVYKRRHVPSSQIMAVKRIRATVNSQEQRLMDIDISMRVDCPPTV 280
 DB 271 ERIDPSASRQGYDVRSDVSLGTITLALIRPPYDSWGPFOQLKOVVEEPSPOLPAD- 330
 QY 281 --KFSAEFVDTSOCLKNSKERPTYPELMOPHFFTLHESKGTDVASFYVLL 331
 DB 331 ERFSPSTINVLNCLTKDESKRPRKYLKHPFLIMTEERTVDVAGYVKIL 383

RESULT 7
 MPK4_HUMAN STANDARD; PRT; 399 AA.

AC P45985;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dual specificity mitogen-activated protein kinase kinase 4
 DE (EC 2.7.1.-) (MAP kinase kinase 4) (JNK activating kinase 1) (C-JUN N-terminal kinase kinase 1) (JUNK) (SAPK/ERK kinase 1) (SEK1).

GN MAP2K4 OR PRKMK4 OR JNK1 OR MKK4 OR SEKK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9523504; PubMed=7716521;
 RA Lin A., Minden A., Martinetto H., Claret F.-X., Lange-Carter C.,
 Mercutio F., Johnson G.L., Karin M.,
 RT "Identification of a dual specificity kinase that activates the Jun
 RT kinases and p38-Mpk2."
 RL Science 268:286-290(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Brain;
 RX MEDLINE=95141073; PubMed=7839144;
 RA Derjard B., Ransgaard J., Barrett T., Wu I.-H., Han J.,
 RT Ulevitch R.J., Davis R.J.;
 RT "Independent human MAP-kinase signal transduction pathways defined by
 RT MEK and MKK isoforms."
 RL Science 267:682-685(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98283389; PubMed=9622070;
 RA Su G.H., Hlgers W., Shekher M.C., Tang D.J., Yeo C.J., Hruban R.H.,
 RT Kern S.E.;
 RT "Alterations in pancreatic, biliary, and breast carcinomas support
 RT MKK4 as a genetically targeted tumor suppressor gene."
 RL Cancer Res. 58:2339-2342(1998).
 RN [4]
 RP CLEAVAGE BY ANTHRAX LETHAL FACTOR.
 RX MEDLINE=20558083; PubMed=11104681;
 RA Vitale G., Bernadi L., Napolitano G., Mock M., Montecucco C.;
 RT "Susceptibility of mitogen-activated protein kinase family
 RT members to proteolysis by anthrax lethal factor."
 RL Biochem. J. 352:739-745(2000).
 CC -1- FUNCTION: DUAL SPECIFICITY KINASE THAT ACTIVATES THE JUN KINASES
 CC MAPK8 (JNK1) AND MAPK9 (JNK2) AS WELL AS MAPK14 (P38) BUT NOT
 CC MAPK1 (ERK2) OR MAPK3 (ERK1).
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IS SEEN IN THE SKELETAL
 CC MUSCLE. IT IS ALSO WIDELY EXPRESSED IN OTHER TISSUES.
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON SER/THR BY MAP KINASE KINASE
 CC KINASES (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- MAP KINASE KINASE SUBFAMILY.
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 CC -----
 CC EMBL: U17743; AAC50127.1; -
 DR EMBL: L36870; AAC41719.1; -
 DR EMBL: AF070090; AAC24130.1; -
 DR EMBL: AF070080; AAC24130.1; JOINED.
 DR EMBL: AF070081; AAC24130.1; JOINED.
 DR EMBL: AF070082; AAC24130.1; JOINED.
 DR EMBL: AF070083; AAC24130.1; JOINED.
 DR EMBL: AF070084; AAC24130.1; JOINED.
 DR EMBL: AF070085; AAC24130.1; JOINED.
 DR EMBL: AF070086; AAC24130.1; JOINED.
 DR EMBL: AF070087; AAC24130.1; JOINED.
 DR EMBL: AF070088; AAC24130.1; JOINED.
 DR EMBL: AF070089; AAC24130.1; JOINED.
 DR GeneW: HGNC:6844; MAP2K4.
 DR MIM: 601335; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.

DR ProDom: PD0000001; Euk_pkinase; 1.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
 KW ATP-binding; Phosphorylation.
 FT DOMAIN 5 19 GLY/SER-RICH.
 FT DOMAIN 102 367 PROTEIN KINASE.
 FT NP_BIND 105 113 ATP (BY SIMILARITY).
 FT BINDING 131 131 ATP (BY SIMILARITY).
 FT ACT_SITE 229 229 BY SIMILARITY.
 FT SITE 45 46 CLEAVAGE (BY ANTHRAX LETHAL FACTOR).
 FT SITE 58 59 CLEAVAGE (BY ANTHRAX LETHAL FACTOR).
 FT SITE 59 59
 SQ SEQUENCE 399 AA; 44287 MW; A472537EF26770B CRC64;
 Query Match 53.18; Score 919; DB 1; Length 399;
 Best Local Similarity 51.38; Pred. No. 5.3e-59;
 Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;
 OY 1 SSGKGRK-----NPKLRPE-----AFEPQTSSTPPRDIDSKACISIG-NQN 44
 DB 35 SSMQGRKALKLNANPPEKSTARFLTNPTGVQNPPIERLRTHSIESGKLTSPQOH 94
 OY 45 FEVKADLEPIMELGRCAYGVVEKMRHVPSCQIANVRKIRATVNSQEQRLMDIDSMR 104
 DB 95 WDFEAEDLKDLGEIGRCAYGVVNMKVPSCQIANVRKIRATVNSQEQRLMDIDVYMR 154
 OY 105 TVDCPFVTVYTGALFRGSDWICMEIMDTSIDKRYK--QYIDKQGITPEDILKIAVSI 161
 DB 155 SSDCPYVQFYGALFRGSDWICMEIMDTSIDKRYK--QYIDKQGITPEDILKIAVSI 212
 OY 162 VKALEHLKSLVTHRDVKNPSNVNLINALGVKMGDFGISGVYVDSVAKTIDAGCKPYAP 221
 DB 213 VKALNHLKENKTIHRDIPNSNILLDRSGNITKLCDFGISGVYVDSVAKTIDAGCKPYAP 272
 OY 222 ERINPELNQKSYKSDWISGIMIEALIRFPVDSMGTPQOLKQVVEEPPSLPAD- 280
 DB 273 ERIPDSASRQGYDVRSDWISGILYELATGFPYPPKNSVFDQLTQYVKGQPPDLSNE 332
 OY 281 --KFSAEVDFDTSCILKKNKSRPTYPPELMQHPFTLHESKTDVAEFYKIL 331
 DB 333 ERESPESTINVNCLTDESKRPYKELKNPFLIWEERAVEACVCKIL 385
 RESULT 8
 ID MPK7_HUMAN STANDARD; PRT; 419 AA.
 AC Q14733; Q14648; O60452; O60453; Q14816;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dual specificity mitogen-activated protein kinase 7
 DE (EC 2.7.1.-) (MAP kinase kinase 7) (MAPKK 7) (MAPK/ERK kinase 7) (JNK
 DE activating kinase 2) (C-Jun N-terminal kinase kinase 2) (JNK kinase 2)
 DE (JUNK 2).
 GN MAP2K7 OR PRKMK7 OR JNK2 OR MKK7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Skeletal muscle, and Heart;
 RX MEDLINE=98038608; PubMed=9372971;
 RA Wu Z., Wu J., Jacinto E., Karin M.;
 RT "Molecular cloning and characterization of human JNK2, a novel Jun
 RT NH2-terminal kinase-specific kinase."
 RL Mol. Cell. Biol. 17:7407-7416(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97460048; PubMed=9312068;
 RA Lu X., Nemoto S., Lin A.;

FT	ACT SITE	243	243	BY SIMILARITY
FT	SITE	44	45	CLEAVAGE (BY ANTHRAX LETHAL FACTOR).
FT	SITE	76	77	CLEAVAGE (BY ANTHRAX LETHAL FACTOR).
FT	VARSPLIC	111	111	Q -> QVPSLWMEGGGAPRLDPSEWROWGAGGGGRADGT
FT	CONFLICT	94	94	LOPSSQ (IN ISOFORM B).
FT	CONFLICT	133	133	Q -> H (IN REF. 2).
FT	CONFLICT	142	142	Q -> P (IN REF. 2).
FT	CONFLICT	259	259	T -> F (IN REF. 1).
SO	SEQUENCE	419 AA;	47485 MM; FIB2E050F54299A CRC64;	L -> F (IN REF. 3).
Query Match				
Best Local Similarity		40.3%;	Score 697;	DB 1; Length 419;
Matches 148; Conservative		42.9%;	Pred. No. 4.8e-43;	
		69;	Mismatches 110;	Indels 18; Gaps 7
QY	1	SOSKGRKRPGLKIKREAEQOTSTPPR----	DISSK-----	ACISIGNONFEVK 48
DB	58	SSSSPPHPPPAPR-PKHMGLPSTLETPRSMESIEIDQKLEIMKOTGYLTIGGORYAK	116	
QY	49	ADDELEIMELGAGVAYKMRHVSQGMAYKRIATVANSQEOKRLMDLDSMTYDC	108	
DB	117	INDLENLGMSGGTCGQYKMKPKRTGHTVAYAKMRSSKNKEENRITLDDLVYKSHDC	176	
QY	109	PPTVTFFGALFREGDVWICMELMDTSIDKFYKQVINDKQITPEDIIDIGIAVSIVALEHL	168	
DB	177	PYVOCGFHTNTDVFETAMELGCAERLKRK--QG-PIPERILGKNTVAIVALLYL	233	
QY	169	HSKLSVIRHDVYKPSVNLINALQYKMCDFGISGYLVDSYAKTIDACKRYMAPERIN-PE	227	
DB	234	KEKHGVINHVDVYKPSNILLDERQIKLDFGIGSRVDSKAKTRRSAGCAAYMAPERIDPPD	293	
QY	228	LNQKGYKSWDMSITMIEALIRFPDYSWGTFPEOOLKOYVEESPQLADK-FSAEF	286	
DB	294	PKRPDYDIRADWMSIGISVELATQGFYKKNCTDTEFLVTLKVLQDEPPLLPHMGFSGDF	353	
QY	287	VDFTSQCLKNSKERPTYPELMQHPFTLHESKGTDVASFYKYL 331		
DB	354	QSFVNDCLTKDHRKRKYNKLLEHFIKRYETLEVDVASWFDVW 398		
RESULT 9				
HEP_DROME				
ID	HEP_DROME	STANDARD:	PRT:	487 AA.
AC	023977;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Dual specificity mitogen-activated protein kinase hemipterous			
DE	(EC 2.7.1.1-) (MARK).			
GN	HEP OR HEM.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
CC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;			
CC	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Oregon-R;			
RX	MEDLINE=96067643; PubMed=8521475;			
RA	Glise B., Bourbon H., Nosselli S.;			
RT	"Hemipterous encodes a novel Drosophila MAP kinase kinase, required			
RT	for epithelial cell sheet movement."			
RL	Cell 83:451-461(1995).			
CC	-1- FUNCTION: REQUIRED FOR THE EPITHELIAL CELL SHEET MOVEMENT CALLED			
CC	DORSAL CLOSURE (DC), WHICH ALLOWS ESTABLISHMENT OF THE DORSAL			
CC	EPIDERMIS. CONTROLS THE EXPRESSION IN THE DORSAL EPITHELIUM EDGES			
CC	-1- PTM: MARK IS ITSELF DEPENDENT ON SER/THR PHOSPHORYLATION FOR			
CC	ACTIVITY CATALYZED BY MAP KINASE KINASE KINASES (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	MAP KINASE KINASE SUBFAMILY.			

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DR EMBL: U05240; AAC46944.1; .
 DR FLYBase: FBgn0010303; hep.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferase: Serine/threonine-protein kinase; Tyrosine-protein kinase;
 KW ATP-binding; Phosphorylation; Developmental protein.
 FT DOMAIN 95 106
 FT NP_BIND 201 209 ATP (BY SIMILARITY).
 FT BINDING 224 224 ATP (BY SIMILARITY).
 FT ACT_SITE 318 318 BY SIMILARITY.
 FT MOD_RES 346 346 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 350 350 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 487 AA; 53079 MW; 09E248DBD14A1E45 CRC64;

Query Match 40.2%; Score 696; DB 1; Length 487;
 Best Local Similarity 44.2%; Pred. No. 6.8e-43;
 Matches 141; Conservative 58; Mismatches 100; Indels 20; Gaps 5;

27 TPRPD-----LDKACISIGNQNEFKADLEPIMLGAGVGEKRRVPS 74
 158 TPRPVPSEFMKLTIMQGTGLNGKQIPYDINDLKLGLGNGTSSNVKMHLS 217
 75 GQIMAVKIRATVNSQEKRLMDLDSMTVDCTPTVFFYGLAFREGDVICMELMDS 134
 218 NTIIVKQMRRTGNMKNRILMDLVLCSDCKIVKCLGCFVRDPVWICMELMSMC 277
 135 LDKFKQVIDKQGTIPEDILKAVSIVALELHLSKLSIYHNDVKSNNVLINAGQVKM 194
 278 FPKRLK-LSK-KPVEQILGKVTAVNALSTYLKKGHGIYHNDVKSNNLIDRGNIKL 334
 195 CGEFGISGLVDSVAKTIDAGCKRYMAPERINPELNOKGYSVKSIDMSLITMELALRF 254
 335 CGEFGISGLVDSKATRSAGCAAYMAPERIDPK-KPKYDIDVMSLGITIVELATARS 392
 255 PYDSWGTTPQOLKQVVEEPPQIPADK---FSAEYVDFTSQCLAKNSKERPTTELMQHP 311
 393 PYEGCMTDFEVLTKVLDSEPPCLPYGEGYMFSDQFRDFVTKLTKRKHQDRKPYELLAQP 452
 312 FTLHESKGDVASFVKLI 330
 453 FRIYESAKVDVPMFQSI 471

RESULT 10
 YR62_CAEEL STANDARD; PRT; 363 AA.
 ID YR62_CAEEL
 AC 020347; 001707;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative serine/threonine-protein kinase F42G10.2 in chromosome II
 DE (EC 2.7.1.1).
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 OX NCBI_TaxID-6239;
 GN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-Bristol N2;
 RA Harris B., Lennard N.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
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DR EMBL: Z95122; CAB08355.1; .
 DR EMBL: Z48230; CAB08355.1; JOINED.
 DR EMBL: Z48230; CAB88264.1; .
 DR EMBL: Z95122; CAB88264.1; JOINED.
 DR WormPep: F42G10.2; CE10328.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
 KW ATP-binding.
 FT DOMAIN 66 330
 FT NP_BIND 72 80 ATP (BY SIMILARITY).
 FT BINDING 95 95 ATP (BY SIMILARITY).
 FT ACT_SITE 194 194 BY SIMILARITY.
 SQ SEQUENCE 363 AA; 41197 MW; 643A26A2329759A CRC64;

Query Match 36.3%; Score 628.5; DB 1; Length 363;
 Best Local Similarity 39.8%; Pred. No. 3.4e-38;
 Matches 136; Conservative 56; Mismatches 111; Indels 39; Gaps 7;

21 QPQTSSTPPRDLDSKACISIGNQ-----FEVADLEPTM 56
 16 RPTSLSTPSTLSVN-----GNEKTLPEESVLSLSTGLTKPPDEHLLTSSANLQDGL 70
 57 ELGGAGVGVEMKRRVPSGQIMAVKIRATVNSQEKRLMDLDSMTVDCTPTVFFYGLAF 115
 71 AIGNCNFTVTKMKRKEGKGLAVKRICNNNGHREQRLLEHNDIVKSEKPNIVKEY 130
 116 GAFREGDVICMELMDSLDEKYQV-IDKQGTIPEDILKAVSIVALELHLSKLSY 174
 131 GAFREGDVICMELMDSLDEKYQV-IDKQGTIPEDILKAVSIVALELHLSKLSY 190
 175 IHRDVKPSNNVLINAGQVKMCDGFGISGLVDSVAKTIDAGCKRYMAPERINPELNOKGYS 234
 191 IHRDVKPSNNVLINAGQVKMCDGFGISGLVDSVAKTIDAGCKRYMAPERINPELNOKGYS 247
 235 VKSDIWSLGLTMIETALIRFPYDSWGTTPQOLKQVVEEPPQIPADK---FSAEYVDF 290
 248 VASDVMISLGLTLYELATGKFPYQEWMSLFDQATVAVSGDPIIHPDSDFHVSILPVKFI 307
 291 SGLKNSKERPTTELMQHPFTLHESKGDVASFVKLI 332
 308 NTLTKRHRHREKPYDLTKSFDYRIYAVAGPEIEE-AKRILG 348

RESULT 11
 WIS1_SCHPO STANDARD; PRT; 605 AA.
 ID WIS1_SCHPO
 AC P33886;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein kinase wisi (EC 2.7.1.1) (protein kinase sty2).
 GN WIS1 OR SPC2 OR STY2 OR SPC409.07C.
 OS Schizosaccharomyces pombe (fission yeast).

RP SEQUENCE OF 91-101 FROM N.A., AND MUTAGENESIS.
 RX MEDLINE=95350642; PubMed=7624781;
 RA Maeda T., Takekawa M., Saito H.;
 RT "Activation of yeast Pbs2 MAPK by MAPKKs or by binding of an SH3-
 containing osmosensor.";
 RL Science 269:554-558(1995).
 RN (5)
 RP FUNCTION.
 RX MEDLINE=93206121; PubMed=7681220;
 RA Brewster J.L., de Valoir T., Dwyer N.D., Winter E., Gustin M.C.;
 RT "An osmosensing signal transduction pathway in yeast.";
 RL Science 259:1760-1763(1993).
 CC -1- FUNCTION: KINASE INVOLVED IN A SIGNAL TRANSDUCTION PATHWAY THAT IS
 CC ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE EXTRACELLULAR
 CC ENVIRONMENT. SEEMS TO PHOSPHORYLATE HOG1 ON A TYROSINE RESIDUE.
 CC -1- DOMAIN: ALTERNATIVE WAY OF ACTIVATION INVOLVES BINDING THE
 CC PROLINE-RICH MOTIF TO THE SH3 DOMAIN OF SHO1.
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION BY SSK2 OR SSK22. SER/THR
 CC PHOSPHORYLATION IS ALSO NECESSARY FOR SHO1-MEDIATED ACTIVATION.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: J02946; AAA16819.1; -
 DR EMBL: U12237; AAA20392.1; -
 DR EMBL: Z49403; CAA89423.1; -
 DR PIR: A32714; A32714.
 DR SGD: S0003664; PBS2.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_ST; 1.
 DR TRANSFERASE: Serine/threonine-protein kinase; Tyrosine-protein kinase;
 KW ATP-binding; Antibiotic resistance; Phosphorylation.
 FT DOMAIN 91 101
 FT NP_BIND 360 623
 FT BINDING 366 374
 FT ACT_SITE 389 389
 FT MOD_RES 485 485
 FT MOD_RES 514 514
 FT MOD_RES 518 518
 FT MUTAGEN 96 96
 FT MUTAGEN 389 389
 FT MUTAGEN 514 514
 FT MUTAGEN 518 518
 FT CONFLICT 222 223
 FT CONFLICT 222 223
 FT CONFLICT 668 668
 FT CONFLICT 668 668
 SQ SEQUENCE 668 AA; 72719 MW; 98C3435BDAFE8019 CRC64;
 YIYICL (IN REF. 1).
 Query Match 35.0%; Score 606; DB 1; Length 668;
 Best Local Similarity 37.3%; Pred. No. 2.9e-36;
 Matches 141; Conservative 73; Mismatches 105; Indels 59; Gaps 12;
 OY 4 KKKRRNGIKI-----PKKAFEPQ-QTSSSTPRDDSK----- 35
 DB 265 EGRKSNFGSLINGVQSTSTSSSTGCPHDYCTTPRTGNSNNSGSGGGLPFANFSKY 324
 OY 36 ACISISGNQNF-----EVKADLLEPIMELGRGAYGVEMKRRHVPSSGQ 76
 DB 325 VDIKSGSLNFAGRKLSKSGKIDFSGSSSRITLDELPLDELGHGNYGNVSKVYLKRPINNV 384

OY 77 IMAKRIRATVNSQEQRLMDLIDSMRTVDCPFVTFYGLAFREGDWICMELMD-TSL 135
 DB 385 IMATKRELRLEDEKFKQIIMLELV-LHKCSPIYVDYGAFFIEGAYVMEYDGGSL 443
 OY 136 DKFYKQVIDKQGITPEDILGKIVASYKALEHLSKLSVIRPDVPSVLINA-LGVYKM 194
 DB 444 DKYDESSSEIG-GIDEPLAFIVANNAVHGLKELEOHNIHRDVPYILNCSANQYKVL 502
 OY 195 CDGEGISGIVDVAKTIDAGCKPYAPERI--NPELNQKGSYKSDIWSIGITMIELAI 251
 DB 503 CDGEGISGIVDVAKTIDAGCKPYAPERI--NPELNQKGSYKSDIWSIGITMIELAI 559
 OY 252 LRFPPY--DSWCTPFOQLKQVVEBSPQPADKFAEYDFTSQCKKSKKEPTPELMO 309
 DB 560 GRYPYPTTYDNIFSQLSAIVDGPPIRPSDFSSDADPVSFLCKIPIRRPTYAALTE 619
 OY 310 HPFTLHESKGTDVASFV 327
 DB 620 HPWLVKYRNQVHMSXYI 637
 RESULT 13
 MKFS_RAT STANDARD: PRT: 448 AA.
 AC Q62862; Q62863; Q62864;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dual specificity mitogen-activated protein kinase 5
 DE (EC 2.7.1.-) (MAP kinase kinase 5) (MAPK 5) (MAPK/ERK kinase 5).
 GN MAP2K5 OR PRKMK5 OR MEK5 OR MKK5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.
 RP STRAIN=Sprague-Dawley; TISSUE=brain;
 RX MEDLINE=96081960; PubMed=7499418;
 RA English J.M., Vanderbilt C.A., Xu S., Marcus S., Cobb M.H.;
 RT "Isolation of MEK5 and differential expression of alternatively
 RT spliced forms.";
 RL J. Biol. Chem. 270:28897-28902(1995).
 CC -1- FUNCTION: INTERACTS SPECIFICALLY WITH ERK5, AND NOT WITH OTHER MAP
 CC KINASES SUCH AS ERK1, ERK2, ERK3, JNK/SAPK, OR P38. IS NOT
 CC PHOSPHORYLATED BY RAF-1, C-MOS, OR MEK1.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (FOR MEK5-BETA) AND PARTICULATE
 CC (MEK5-ALPHA). THE ALTERNATIVELY SPLICED EXON IN ALPHA ISOFORM
 CC RESEMBLE CONSERVED SEQUENCES THAT MEDIATE INTERACTIONS WITH THE
 CC CYTOSKELETON, THEREBY EXPLAINING THE DIFFERENTIAL LOCALIZATION.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: ALPHA-1 (SHOWN HERE), ALPHA-
 CC 2 AND BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: MEK5 BETA IS UNIBOUDOUSLY DISTRIBUTED WITH
 CC HIGHEST LEVELS IN THE LIVER, WHEREAS MEK5 ALPHA IS EXPRESSED ONLY
 CC IN LIVER AND BRAIN.
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON SER/THR BY MAP KINASE KINASE
 CC KINASES (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: U37462; AAC52320.1; -
 DR EMBL: U37463; AAC52321.1; -
 DR EMBL: U37464; AAC52322.1; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000270; Octpept_motif.

InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00564; OPR; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00016; OPR; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
 KM ATP-binding; Phosphorylation; Alternative splicing.
 FT DOMAIN 166 419
 FT NP_BIND 172 180
 FT BINDING 193 180
 FT ACT_SITE 283 283
 FT MOD_RES 311 311
 FT MOD_RES 315 315
 FT VARSPIC 349 358
 FT VARSPIC 311 311
 FT MUTAGEN 315 315
 FT MOTAGEN 315 315
 SQ SEQUENCE 448 AA; 50197 MW; 1B1CC8B05789B90D CRC64;

Query Match 33.9%; Score 587.5; DB 1; Length 448;
 Best local similarity 42.7%; Pred. No. 3.ee-35;
 Matches 144; Conservative 53; Mismatches 111; Indels 29; Gaps 11;

5 GKRRNDGLKIPKFAEPQPTSTPPRDLDSKACISIGNQNEVKADLEPIREL 58
 113 GERINHGKVNFRAGSPQHSPTVSDSPNSLKSSEAEKILANQOMEDIRYDTL 172
 59 GKGAVGVKMRVPSGQIMAVRIRATVNSQDQKRLMDJISMRTVDFVTYFGAL 118
 173 GKGNGTVKRAVHPGSKILAVKILDLTLELOKQIMSELELYCDDSYILGFGAF 231
 119 FREGDWIMELMD-TSLDEKYQVIDKQGTPEIDIGKATVAKLEHLHSLSTYHR 177
 232 FVENRISICTEFMDGSLDYLR-----DEHVLGRAVAVVKKLTLMWS-LKILHR 282
 178 DVKPSNVLINALGVQVMDGSGISGLYVDVAKTIDAGCKPYMAPERINPELNQGSVKS 237
 283 DVKPSNVLAVNTSGQVLCDFGVSQTLVNSIAKTY-VGTNAYMAPERISGE---QYIHS 337
 238 DWSGIGTMIELALIRFV---DSWGT--PFQQLQVVEEPPQLPADFFSAEFVDTLS 291
 338 DWSGIGTMIELALIRFV---DSWGT--PFQQLQVVEEPPQLPADFFSAEFVDTLS 291
 292 QCLKRSKERPTYPELMQHPFTT-LHESKGTDVASPV 327
 398 QCMRKQKRPAPAEELMGHPIVQFMDGNATVYSMV 434

RESULT 14
 MPK1_HUMAN STANDARD; PRT; 392 AA.
 AC Q02750;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dual specifically mitogen-activated protein kinase kinase 1
 DE (EC 2.7.1.-) (Map kinase kinase 1) (MEK1)
 DE (MAPK/ERK kinase 1) (MEK1).
 GN MAP2K1 OR PRKMK1 OR MEK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCB1_TaxID=9606;
 RN (1)
 RP MEDLINE-93100262; PubMed-1281467;
 RA Seger R., Seger D., Lozeman F.J., Ahn N.G., Graves L.M.,
 RA Campbell J.S., Ericsson L., Harrylock M., Jensen A.M., Krebs E.G.;
 RT "Human T-cell mitogen-activated protein kinase kinases are related to
 yeast signal transduction kinases.";

RL J. Biol. Chem. 267:25628-25631(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93266604; PubMed-8388392;
 RA Zheng C.-F., Guan K.-L.;
 RT "Cloning and characterization of two distinct human extracellular
 signal-regulated kinase activator kinases, MEK1 and MEK2."
 RL J. Biol. Chem. 268:11435-11439(1993).
 RN [3]
 RP PHOSPHORYLATION OF SER-217 AND SER-221, AND MUTAGENESIS.
 RX MEDLINE-94178255; PubMed-8131746;
 RA Zheng C.-F., Guan K.-L.;
 RT "Activation of MEK family kinases requires phosphorylation of two
 conserved Ser/Thr residues."
 RL EMBO J. 13:1123-1131(1994).
 RN [4]
 RP CLEAVAGE BY ANTHRAX LETHAL FACTOR, AND SEQUENCE OF 8-16.
 RX MEDLINE-98230732; PubMed-9563949;
 RA Duesbery N.S., Webb C.P., Leppia S.H., Gordon V.M., Klimpel K.R.,
 RA Copeland T.D., Ahn N.G., Oskarsson M.K., Fukasawa K., Paul K.D.,
 RA Vande Woude G.F.;
 RT "Proteolytic inactivation of MAP-kinase-kinase by anthrax lethal
 factor."
 RL Science 280:734-737(1998).
 RN [5]
 RP CLEAVAGE BY ANTHRAX LETHAL FACTOR.
 RX MEDLINE-20558083; PubMed-11104681;
 RA Vitale G., Bernardi L., Napolitani G., Mock M., Montecucco C.;
 RT "Susceptibility of mitogen-activated protein kinase kinase family
 members to proteolysis by anthrax lethal factor."
 RL Biochem. J. 352:739-745(2000).
 CC -1- FUNCTION: CATALYZES THE CONCOMITANT PHOSPHORYLATION OF A THREONINE
 AND A TYROSINE RESIDUE IN A THR-GLU-TYR SEQUENCE LOCATED IN MAP
 KINASES. ACTIVATES ERK1 AND ERK2 MAP KINASES.
 CC -1- PTM: MAPK IS ITSELF DEPENDENT ON SER/THR PHOSPHORYLATION FOR
 ACTIVITY CATALYZED BY MAP KINASE KINASE KINASES (RAF OR MEK1).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: L05624; AAA6318.1; -
 DR EMBL: L11284; -; NOT_ANNOTATED_CDS.
 DR PIR: A45100; A45100.
 DR HSP: 000534; 1B1F8.
 DR Genew: HGNC:6840; MAP2K1.
 DR MIM: 176872; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
 KM ATP-binding; Phosphorylation.
 FT INTL MET 0
 FT DOMAIN 0
 FT NP_BIND 67 360
 FT BINDING 73 81
 FT ACT_SITE 96 96
 FT MOD_RES 189 189
 FT MOD_RES 217 217
 FT MOD_RES 221 221
 FT DOMAIN 261 306
 FT SITE 7 8
 FT MOTAGEN 96 96

BY SIMILARITY.
 PROTEIN KINASE.
 ATP (BY SIMILARITY).
 BY SIMILARITY.
 PHOSPHORYLATION (BY RAF).
 PHOSPHORYLATION (BY RAF).
 PRO-RICH.
 CLEAVAGE (BY ANTHRAX LETHAL FACTOR).
 K->R: INACTIVATION.

FT MTAGN 149 149 S->A: NO LOSS OF ACTIVITY.
 FT MTAGN 211 211 S->A: NO LOSS OF ACTIVITY.
 FT MTAGN 217 217 S->A: INACTIVATION.
 FT MTAGN 221 221 S->A: INACTIVATION.
 SO SEQUENCE 392 AA; 43307 MW; EF7194F7DA698734 CRC64;

Query Match 33.9%; Score 587; DB 1; Length 392;
 Best Local Similarity 38.0%; Pred. No. 3.5e-35;
 Matches 125; Conservative 62; Mismatches 90; Indels 52; Gaps 7;

QY EVKADDDLEPIMELGAGVGEKMRHVPESGQIMAVKIRATVNSOQRLLMDLISMRT 105
 DB ELKDDDFEKISELNGNGVGVKSHKSGVLMARKLHLEIKPAIRNOIIRLOV-LHE 119
 QY 106 VDCPTVTFYALFREGDWTICMELMD-TSLDKFYQVYDKGQITPEDIIGKIAVSIVA 164
 DB 120 CNSPIYGVGAFYSDGEISICMEHMDGSLD---QVLKAGRIPEQLIGKIASIVIKG 175
 QY 165 LEHLSKLSVTHRDVPSNVILNALGOVMKDFGISGVYDSVAKTIDAGCKPYMAPERI 224
 DB 176 LTYLEKHKIMHRDVPKPSNVLNSKGEIKLCPFGVSGQLIDSMANSF-VGTRSYMSPER 233
 QY 225 NPELNOKGYSVKSDIWSLGTIMELAILRPY-----DSWGRP----- 262
 DB 234 ---LQGTHTSVQSDIWSMGLSLVEMAVGRYPIPPPAKLELMFGCQVEGDAEETPRPR 290
 QY 263 -----FOOLKOVVEEPPSLPADKSAEVDFTSCLKRNKSRPT 303
 DB 291 TPGRPLSSYGMDSRPMALFELLDYVNEPPPLPSGVPSLEFQDVFYVNCCLINPARAD 350
 QY 304 YPELMOHPFTLHESKGTVDVASFVKILIG 332
 DB 351 LKQIMVHAFIKRSDAEVDVAFAGWLCSTIG 379

RESULT 15
 MK1 MOUSE STANDARD; PRT; 392 AA.
 ID MK1 MOUSE
 AC P31938;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dual specificity mitogen-activated protein kinase kinase 1
 DE (EC 2.7.1.-) (MAP kinase kinase 1) (MAPKK 1) (ERK activator kinase 1)
 DE (MAPK/ERK kinase 1) (MEK1).
 GN MAP2K1 OR PRKMK1 OR MEK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN RN
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=93030761; PubMed=1411546;
 RA Crews C.M., Alessandrini A., Erikson R.L.;
 RT "The primary structure of MEK, a protein kinase that phosphorylates
 RT the ERK gene product."
 RL Science 258:478-480(1992).
 RN [2]
 RP SEQUENCE OF 3-19; 70-83; 113-135; 205-233 AND 362-383.
 RC TISSUE=T-cell;
 RX MEDLINE=92390415; PubMed=1381507;
 RA Crews C.M., Erikson R.L.;
 RT "Purification of a murine protein-tyrosine/threonine kinase that
 RT phosphorylates and activates the Erk-1 gene product: relationship to
 RT the fission yeast byr1 gene product."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8205-8209(1992).
 RN [3]
 RP CLEAVAGE BY ANTHRAX LETHAL FACTOR.
 RX MEDLINE=98230732; PubMed=956349;
 RA Duesbery N.S., Webb C.P., Leppia S.H., Gordon V.M., Klimpel K.R.,
 RA Copeland T.D., Ahn N.G., Oskarsson M.K., Fukasawa K., Pauli K.D.,
 RA Vande Woude G.F.;
 RT "Proteolytic inactivation of MAP-kinase-kinase by anthrax lethal

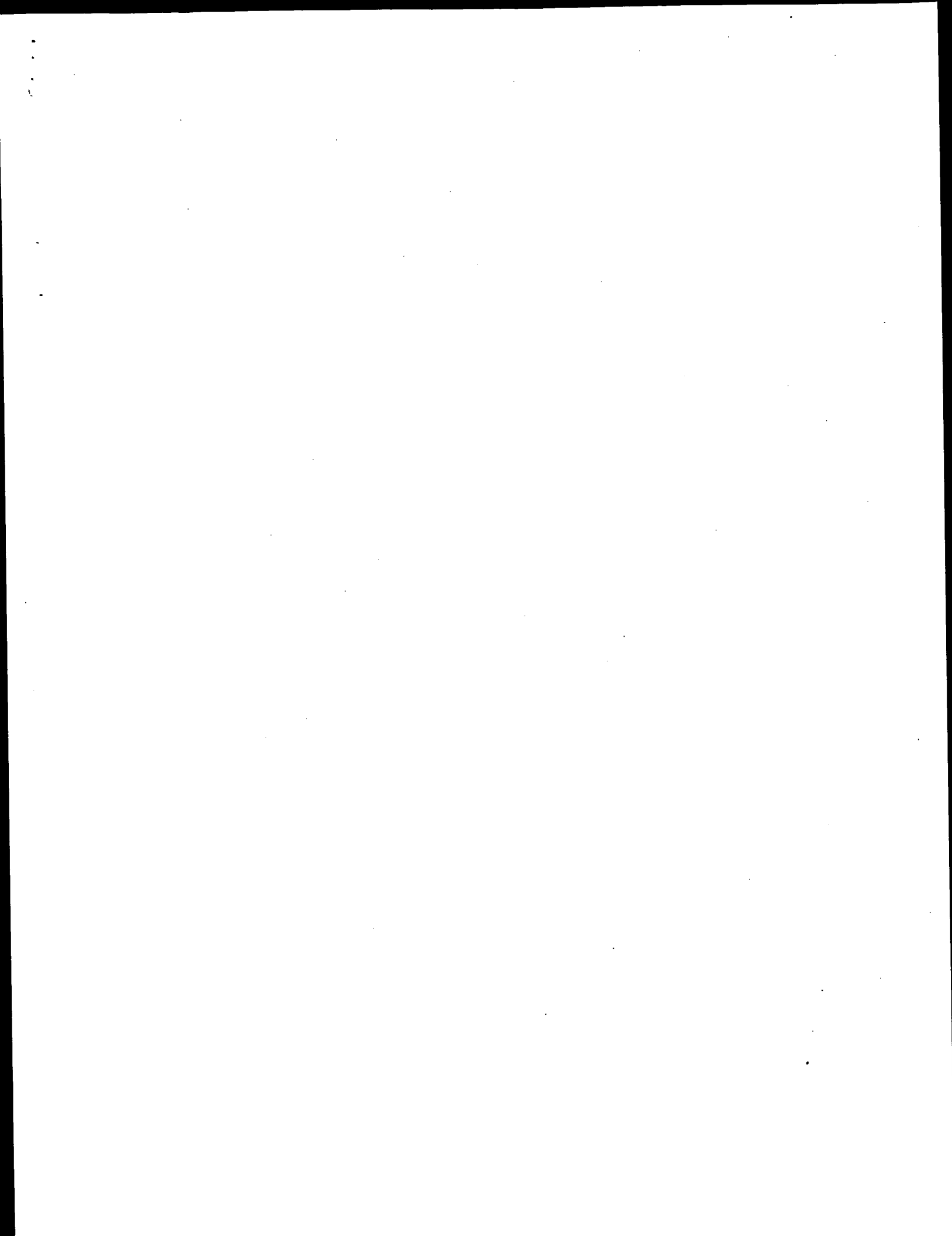
RT factor." Science 280:734-737(1998).
 RL Science 280:734-737(1998).
 CC -1- FUNCTION: CATALYZES THE CONCOMITANT PHOSPHORYLATION OF A THREONINE
 CC AND A TYROSINE RESIDUE IN A THR-GLU-TYR SEQUENCE LOCATED IN MAP
 CC KINASES. ACTIVATES ERK1 AND ERK2 MAP KINASES.
 CC -1- ENZYME REGULATION: INHIBITED BY SERINE/THREONINE PHOSPHATASE 2 A.
 CC -1- PTM: MARK IS ITSELF DEPENDENT ON SER/THR PHOSPHORYLATION FOR
 CC ACTIVITY CATALYZED BY MAP KINASE KINASE KINASES (RAF OR MEK1).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: L02526; AAA39523.1; -.
 CC HSP: Q00534; 1B18.
 CC MGD: MGI:1346866; Map2K1.
 CC InterPro: IPR000719; Euk_Pkinase.
 CC InterPro: IPR002290; Ser_thr_Pkinase.
 CC Pfam: PF00065; Pkinase; 1.
 CC ProDom: PD000001; Euk_Pkinase; 1.
 CC SMART: SM00220; S_TKC; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC DR transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
 CC ATP-binding; Phosphorylation.
 CC BY SIMILARITY.
 CC INIT_MET 0
 CC DOMAIN 0
 CC NP_BIND 67 360
 CC NP_BIND 73 81
 CC BINDING 96 96
 CC ACT_SITE 189 189
 CC MOD_RES 217 217
 CC MOD_RES 221 221
 CC DOMAIN 261 306
 CC SITE 7 8
 CC CLEAVAGE (BY ANTHRAX LETHAL FACTOR) (BY
 CC SIMILARITY).
 CC W -> Q (IN REF. 2).
 SO SEQUENCE 392 AA; 43343 MW; EDE454FD543EAB2 CRC64;
 Query Match 33.9%; Score 587; DB 1; Length 392;
 Best Local Similarity 38.0%; Pred. No. 3.5e-35;
 Matches 125; Conservative 62; Mismatches 90; Indels 52; Gaps 7;
 QY EVKADDDLEPIMELGAGVGEKMRHVPESGQIMAVKIRATVNSOQRLLMDLISMRT 105
 DB ELKDDDFEKISELNGNGVGVKSHKSGVLMARKLHLEIKPAIRNOIIRLOV-LHE 119
 QY 106 VDCPTVTFYALFREGDWTICMELMD-TSLDKFYQVYDKGQITPEDIIGKIAVSIVA 164
 DB 120 CNSPIYGVGAFYSDGEISICMEHMDGSLD---QVLKAGRIPEQLIGKIASIVIKG 175
 QY 165 LEHLSKLSVTHRDVPSNVILNALGOVMKDFGISGVYDSVAKTIDAGCKPYMAPERI 224
 DB 176 LTYLEKHKIMHRDVPKPSNVLNSKGEIKLCPFGVSGQLIDSMANSF-VGTRSYMSPER 233
 QY 225 NPELNOKGYSVKSDIWSLGTIMELAILRPY-----DSWGRP----- 262
 DB 234 ---LQGTHTSVQSDIWSMGLSLVEMAVGRYPIPPPAKLELMFGCQVEGDAEETPRPR 290
 QY 263 -----FOOLKOVVEEPPSLPADKSAEVDFTSCLKRNKSRPT 303
 DB 291 TPGRPLSSYGMDSRPMALFELLDYVNEPPPLPSGVPSLEFQDVFYVNCCLINPARAD 350
 QY 304 YPELMOHPFTLHESKGTVDVASFVKILIG 332
 DB 351 LKQIMVHAFIKRSDAEVDVAFAGWLCSTIG 379

Fri Jun 6 15:36:19 2003

us-09-593-288-2.rsp

Page 13

Search completed: June 6, 2003, 09:10:47
Job time : 13 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 09:05:58 ; Search time 32 Seconds

(without alignments)
2144.178 Million cell updates/sec

Title: US-09-593-288-2

Perfect score: 1731
Sequence: 1 SOSGKRRNPGLKIPKEAFE.....TLHESKGTDVASFVKLLIGD 333

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1699	98.2	334	11	Q925D6
2	1583.5	91.5	335	13	Q9PW48
3	1523	88.0	404	13	Q91959
4	1495.5	86.4	363	13	Q9DGE0
5	1384	80.0	347	4	Q9UW72
6	1383	79.9	347	4	Q9UW72
7	1370	79.1	347	11	Q9UW72
8	1370	79.1	352	4	Q9UW72
9	1221	70.5	237	11	Q60521
10	1036	59.8	335	5	Q9UW83
11	1034	59.7	334	5	Q62602
12	936.5	54.1	407	13	Q8UW90
13	870.5	50.3	336	5	Q95Y19
14	865.5	50.0	343	5	Q21669
15	850	49.1	281	13	Q9DGR7
16	835.5	48.3	424	5	O61444

17	822	47.5	162	11	P70273
18	697.5	40.3	492	5	O18411
19	697.5	40.3	1178	5	O8S221
20	694	40.1	389	11	O35720
21	694	40.1	391	11	O35872
22	694	40.1	419	11	O35871
23	694	40.1	435	11	O35871
24	694	40.1	468	11	O54780
25	693.5	40.1	356	5	O95U55
26	692.5	40.0	417	13	O80HK7
27	690.5	39.9	453	11	O9R124
28	690.5	39.9	469	11	O9R126
29	688.5	39.8	346	11	O9QW66
30	685	39.6	380	11	O9R123
31	682.5	39.4	346	11	O35406
32	618	35.7	359	5	O01706
33	610.5	35.3	505	5	O21307
34	588	34.0	400	11	O91YS7
35	587.5	33.9	401	11	O9D7B0
36	587.5	33.9	448	11	O9WVS7
37	587	33.9	393	11	O9JTE1
38	584	33.7	448	4	O92961
39	577	33.3	173	11	O91YX1
40	575.5	33.2	683	3	O96W50
41	575	33.2	393	6	O9XU09
42	564	32.6	371	5	O23326
43	563	32.5	397	13	O8UW89
44	553	31.9	451	4	O92962
45	542	31.3	396	5	O9W360

ALIGNMENTS

RESULT 1	
ID	Q925D6
AC	Q925D6
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE	Mitogen-activated protein kinase kinase 6.
GN	MKK6
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY;
RA	Glembowski C.C., Smith L.M., Therauf D.J., Monia B.P., Craig R.A.;
RL	Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF639384; AAK53428.1;
DR	InterPro: IPR000719; Euk_pkinase.
DR	InterPro: IPR002290; Ser_thr_pkinase.
DR	InterPro: IPR001245; Tyr_pkinase.
DR	Pfam: PF00069; pkinase; 1.
DR	ProDom: PD000001; Euk_pkinase; 1.
DR	SMART: SM00219; TyrKc; 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW	ATP-binding; Kinase; Transferase.
SEQ	SEQUENCE 334 AA: 37444 MW: C6A4843F82P63D87 CRC64;
QY	Query Match 98.2%; Score 1699; DB 11; Length 334;
DB	Best Local Similarity 97.3%; Pred. No. 4e-138;
	Matches 324; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
	1 SOSGKRRNPGLKIPKEAFEQPTSTPPRDLDSKACISIGNQNEVKKADLEPIVELGR 60
	2 SOSGKRRNPGLKIPKEAFEQPTSTPPRDLDSKACISIGNQNEVKKADLEPIVELGR 61

ID Q9DGE0 PRELIMINARY; PRT; 363 AA.
 AC Q9DGE0;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE MKK3.
 GN MAP2K3 OR ZMKK3.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 NCBI_TaxID=7935;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20451058; PubMed=10995439;
 RA Fujii R., Yamashita S., Hibi M., Hirano T.;
 RT "Asymmetric p38 Activation in Zebrafish: Its Possible Role in
 RT Symmetric and Synchronous Cleavage";
 RL J. Cell Biol. 150:1335-1348(2000).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AB030899; BAB11809.1; -;
 DR ZFIN; ZDB-GENE-010202-3; map2k3.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002230; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase;
 SQ SEQUENCE 363 AA; 40807 MW; 02A7CD9A6F5A2DC CRC64;

Query Match 86.4%; Score 1495.5; DB 13; Length 363;
 Best Local Similarity 87.0%; Pred. No. 1.5e-120;
 Matches 288; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

QY 4 KKKRRNP-GIKPIKEAFEPOTSSTPRDLSKACISIGNONFEVKADLEPIMELGR 62
 DB 33 RKKKRLPKRELKPEKFEKAPAPTPPRDLSKAYVITIGENFVKKADLEIGELGR 92
 QY 63 YGVVERKMRHVPSCQINAVKRIRATVNSQEQRLMDIDISRTVDCPPTVFGALFR 122
 DB 93 YGVVDRMRHVPSCQINAVKRIRATVNTQEQRLMDIDISRTVDCPPTVFGALFR 152
 QY 123 DWIMICELMDTSLDKRYKQYIDKGQITPEDILGKINAVKALEHLSKLSYIHRDVK 182
 DB 153 DWIMICELMDTSLDKRYKQYIDKGQITPEDILGKISIVKALEHLSNLSYIHRDVK 212
 QY 183 NVLINAGVKKMCDGFGISGYLVDSVAKTIDAGCKPYAPERINPELNOKGYSVKSDI 242
 DB 213 NVLINAGVKKMCDGFGISGYLVDSVAKTIDAGCKPYAPERINPELNOKGYSVKSDI 272
 QY 243 GITMIELALIRPYDSMGTPFQOLKQVVEEPPOLPADKFSAEVDFTSQCLKKNSKE 302
 DB 273 GITMIELALIRPYDSMGTPFQOLKQVVEEPPOLPADKFSAEVDFTSQCLKKNSKE 332
 QY 303 TYPELMQHPFTLHESKGTVDVAFVKILID 333
 DB 333 TYPELMQHPFTLHESKGTVDVAFVKILID 363

RESULT 5

Q9UE72 PRELIMINARY; PRT; 347 AA.
 AC Q9UE72;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE MAP kinase 3b.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Han Jianhui;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; U66839; A840652.1; -;
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002230; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 347 AA; 39317 MW; A80BA4FDF8F7D82 CRC64;

Query Match 80.0%; Score 1384; DB 4; Length 347;
 Best Local Similarity 80.2%; Pred. No. 5.7e-111;
 Matches 267; Conservative 33; Mismatches 31; Indels 2; Gaps 2;

QY 2 QSKGR-KRNPGLIKPEAFEPOTSSTPRDLSKACISIGNONFEVKADLEPIMELGR 60
 DB 14 QSKGRKKKKDLRLSCMS-KPPAPPTPRRNDLSRTFITIGDNFVEADDLVTISLGR 72
 QY 61 GAYGVVERKMRHVPSCQINAVKRIRATVNSQEQRLMDIDISRTVDCPPTVFGALFR 120
 DB 73 GAYGVVERKMRHVPSCQINAVKRIRATVNSQEQRLMDIDISRTVDCPPTVFGALFR 132
 QY 121 EGDWIMICELMDTSLDKRYKQYIDKGQITPEDILGKINAVKALEHLSKLSYIHRDVK 180
 DB 133 EGDWIMICELMDTSLDKRYKQYIDKGQITPEDILGKISIVKALEHLSNLSYIHRDVK 192
 QY 181 PSNVLINAGVKKMCDGFGISGYLVDSVAKTIDAGCKPYAPERINPELNOKGYSVKSDI 240
 DB 193 PSNVLINAGVKKMCDGFGISGYLVDSVAKTIDAGCKPYAPERINPELNOKGYSVKSDI 252
 QY 241 SLGITMIELALIRPYDSMGTPFQOLKQVVEEPPOLPADKFSAEVDFTSQCLKKNSKE 300
 DB 253 SLGITMIELALIRPYDSMGTPFQOLKQVVEEPPOLPADKFSAEVDFTSQCLKKNSKE 312
 QY 301 RPTYPELMQHPFTLHESKGTVDVAFVKILID 333
 DB 313 RPTYPELMQHPFTLHESKGTVDVAFVKILID 345

RESULT 6

Q99441 PRELIMINARY; PRT; 347 AA.
 AC Q99441;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE MAP kinase kinase 3b.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Moriyuchi T., Toyoshima F., Gotoh Y., Iwamatsu A., Irie K., Mori E.,
 RA Kuroyanagi N., Hagiwara M., Matsumoto K., Nishida E.;
 RT "Purification and Identification of a major activator for p38 from
 RT osmotically shocked cells. Activation of MAPK6 by osmotic shock,
 RT tumor necrosis factor-alpha and H2O2.";
 RL J. Biol. Chem. 0:0-0(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9705154; PubMed=8900184;
 RA Moriyuchi T., Toyoshima F., Gotoh Y., Iwamatsu A., Irie K., Mori E.,
 RA Kuroyanagi N., Hagiwara M., Matsumoto K., Nishida E.;

RESULT 8

09UE71 PRELIMINARY; PRT; 352 AA.

AC 09UE71: TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE MAP kinase 3c.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RA SEQUENCE FROM N.A.

RP Han Jiahui;

RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; U66840; AAB40653.1; -

DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR Prodom; PD000001; Euk_pkinase; 1.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 352 AA; 39939 MW; F59612D9001E1E5 CRC64;

Query Match 79.18; Score 1370; DB 4; Length 352;

Best Local Similarity 80.0%; Pred. No. 9.3e-110;

Matches 264; Conservative 33; Mismatches 31; Indels 2; Gaps 2;

QY 5 GK-KRNGKIKPKAFPOQSSPPRLDLSKACISIGNONPEYKADLEPIEMELGAY 63

DB 22 GKSKRRKDLKISCMS-KRPADNPPIPRNLDLSRTFTIGDRNEFEADLVVISLGRGAY 80

QY 64 GVEVKMRHVSQGITMAVKRIRATVNSOEOKRLMDLDSMTVDCPFTVTYFGALFREGD 123

DB 81 GVEKRYHAQSQTIMAVKRIRATVNSOEOKRLMDLDSMTVDCPFTVTYFGALFREGD 140

QY 124 VVICMELMDTSLDKFYQVVDKGTIPEDILGKTAIVSIVKALEHLHSLKSVIHRDKPSN 183

DB 141 VVICMELMDTSLDKFYKRVLDKNTIPEDILGKTAIVSIVKALEHLHSLKSVIHRDKPSN 200

QY 184 VLINAGOVKMGCEFGISGYLVDSYAKTIDAGCKRYMAPERINPELNOKGYVSKDSVSLG 243

DB 201 VLINKGHVAKMCPFGISGYLVDSYAKTIDAGCKRYMAPERINPELNOKGYVSKDSVSLG 260

QY 244 ITWIELALIRFPYDSWGTPOOLKOVVEEESPOLPADKFSAEFVDFTSOCLKNSKERPT 303

DB 261 ITWIELALIRFPYDSWGTPOOLKOVVEEESPOLPADKFSAEFVDFTSOCLKNSKERPT 320

QY 304 YPELMQHPFTLHESGTDVASFVKILGD 333

DB 321 YPELMQHPFTLHESGTDVASFVKILGE 350

RESULT 9

060521 PRELIMINARY; PRT; 237 AA.

AC 060521: TREMBLrel. 01, Created)

DT 01-MAY-1996 (TREMBLrel. 01, Last sequence update)

DT 01-MAY-1996 (TREMBLrel. 01, Last sequence update)

DE MAP kinase 6c.

GN MAPK6.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96216353; PubMed=8621675;

RX Han J., Lee J.D., Jiang Y., Li Z., Feng L., Ulevitch R.J.;

RT "Characterization of the structure and function of a novel MAP kinase (MKK6).";

RT Kinase (MKK6).";

RL J. Biol. Chem. 271:2886-2891(1996).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; U39066; AAB03709.1; -

DR MGI; MGI:1346870; Map2k6.

DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR Prodom; PD000001; Euk_pkinase; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 237 AA; 26691 MW; 17D945B25D908B45 CRC64;

Query Match 70.58; Score 1221; DB 11; Length 237;

Best Local Similarity 97.5%; Pred. No. 3.7e-97;

Matches 231; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 97 MDLDSKRTVDCPFTVTFYGLFREGDVCWICMELMDTSLDKFYQVVDKGTIPEDILGK 156

DB 1 MDLDSKRTVDCPFTVTFYGLFREGDVCWICMELMDTSLDKFYQVVDKGTIPEDILGK 60

QY 157 IAVSIVKALEHLHSLKSVIHRDKPSNVLINAGOVKMGCEFGISGYLVDSYAKTIDAGCK 216

DB 61 IAVSIVKALEHLHSLKSVIHRDKPSNVLINAGOVKMGCEFGISGYLVDSYAKTIDAGCK 120

QY 217 PYMAPERINPELNOKGYSVKSDVSLGITWIELALIRFPYDSWGTPOOLKOVVEESPQ 276

DB 121 PYMAPERINPELNOKGYSVKSDVSLGITWIELALIRFPYDSWGTPOOLKOVVEESPQ 180

QY 277 LPADKFSAEFVDFTSOCLKNSKERPTPELMQHPFTLHESGTDVASFVKILGD 333

DB 181 LPADKFSAEFVDFTSOCLKNSKERPTPELMQHPFTLHESGTDVASFVKILGD 237

RESULT 10

090983 PRELIMINARY; PRT; 335 AA.

AC 090983: TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE MAPK.

GN LIC OR LICORNE OR CG12244.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RA SEQUENCE FROM N.A.

RP Suzanne M., Title K., Glise B., Agnes F., Mori E., Matsumoto K., Noselli S.;

RT "The Drosophila p38 MAPK pathway is required during oogenesis for egg asymmetric development.";

RL Genes Dev. 13:1464-1474(1999).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AJ238572; CAB45101.1; -

DR Flybase; FBgn0015763; lic.

DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR Prodom; PD000001; Euk_pkinase; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Serine/threonine-protein kinase; Transferase.

SEQUENCE 335 AA; 38195 MW; FD31C46ECB95F1BE CRC64;

QY 320 GIVVAFVKLIL 331
 Db 314 NTDISEFVARIL 325

RESULT 12

Q80W90 PRELIMINARY; PRT; 407 AA.
 AC 080W90;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE MAP kinase kinase 4.
 GN CMK4.
 OS Cyrtinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_Taxid=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hashimoto H.;
 RT "Carp MKK4";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB063389; BAB79524.1;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Prodom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 DR KINASE.
 SQ SEQUENCE 407 AA; 46091 MW; 3A178B6C24867CCB CRC64;

Query Match

Best Local Similarity 54.1%; Score 936.5; DB 13; Length 407;
 Matches 185; Conservative 56; Mismatches 88; Indels 27; Gaps 6;

QY 2 OSKGRK-----NPKL-----IPKEAFEPQTSSTPRDLDSKACISIG- 41
 Db 43 QSDSGKRAKLKLNFPNPPKPTSRITLNTAGLP---FQNPHERLRTHSIESGKLIKSP 99
 QY 42 NQFEVKADLEPIIMELRGAYGVYKMRHVPSSGOIMAYKRIRATYVNSQOKRLMDLDI 101
 Db 100 EQHMFPTADLKDLEIGGAYGVYKMRHVPSSGOIMAYKRIRATYVNSQOKRLMDLDV 159
 QY 102 SMRTVDCPFTVTFYCALFREGGDWICMELMDTSLDKFYKQVIDK-GQTTPEIDILGKIAVS 160
 Db 160 VMRSDDCPYIVQFYCALFREGGDWICMELMDTSLDKFYKQVIDK-GQTTPEIDILGKIAVS 219
 QY 161 IVKALEHLSKLSVHRDVPKSNVILNAGVYKMRHVPSSGOIMAYKRIRATYVNSQOKRLMDLDI 220
 Db 220 TVKALNHLKEMKIKTHIDKPSNILLDRKGNITLDFGISGOLVDSIAKTRDAGCRPYMA 279
 QY 221 PERINPELNOKGYKSDIWSIGITMELAILRFPYDSGTPFOOLKQVVEEESPOLPAD 280
 Db 280 PERIDPSASRGQYDRSDVWSIGITLTLATGRFRFPKNSVFDOLTVQVKGDPOLSSS 339
 QY 281 ---KFAEFVDFTSOCLKKNKSKERPTYPELMOHPEFTLHESKGTIVASFKLILGD 333
 Db 340 EERQFSPTFINVNLCTKESKSRPKYKELKHPTIOWMEERTVDVASYVCKILDE 395

RESULT 13

Q95Y19 PRELIMINARY; PRT; 336 AA.
 AC 095Y19;
 DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE MAP kinase kinase SEK-1.
 GN SEK-1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
 OC Rhabdilitida; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanaka-Hino M., Sagasti A., Hisamoto N., Kawasaki M., Nakano S.,
 RA Niinomiya-Tsujii J., Bargmann C.I., Matsumoto K.;
 RT "Caklii-p38/MAPK pathway that determines neuronal asymmetric
 development in C.elegans";
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB060731; BAB43977.2;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Prodom: PD000001; Euk_pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 DR ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 336 AA; 38700 MW; 5E5E4EFLCC374FA0 CRC64;

Query Match

Best Local Similarity 50.3%; Score 870.5; DB 5; Length 336;
 Matches 170; Conservative 64; Mismatches 90; Indels 11; Gaps 6;

QY 2 OSKGRKRN-PGLKIRKEAFEPQTSSTPRDLDSKACISIGNON--FEVKADLEPIIMEL 58
 Db 2 ERKGRKRLPKMKI-----VMPPTVETPRMNLDRCLILTESEIEELIATLVLVEEL 56
 QY 59 GRGAYGVYKMRHVPSSGOIMAYKRIRATYVNSQOKRLMDLISMTVDCPFTVTFYCAL 118
 Db 57 GKGYGVYKMRHVPSSGOIMAYKRIRATYVNSQOKRLMDLISMTVDCPFTVTFYCAL 116
 QY 119 FREGDWICMELMDTSLDKFYKQVIDKQTTPEIDILGKIAVSIVKALEHLSKLSVHRD 178
 Db 117 FREGDWICMELMDTSLDKFYKQVIDKQTTPEIDILGKIAVSIVKALEHLSKLSVHRD 176
 QY 179 VKPSNVILNAGVYKMRHVPSSGOIMAYKRIRATYVNSQOKRLMDLISMTVDCPFTVTFYCAL 238
 Db 177 VKPSNVILNAGVYKMRHVPSSGOIMAYKRIRATYVNSQOKRLMDLISMTVDCPFTVTFYCAL 235
 QY 239 IWSIGITMELAILRFPYDSGTPFOOLKQVVEEESPOLPADK-FSAEFVDFTSOCLKKN 297
 Db 236 VWSIGITMELAILRFPYDSGTPFOOLKQVVEEESPOLPADK-FSAEFVDFTSOCLKKN 295
 QY 298 SKERTYPELMOHPEFTLHESKGTIVASFKLIL 331
 Db 296 YNERPKYPELMAMPMEQARNEKPSMARFIEL 330

RESULT 14

Q21669 PRELIMINARY; PRT; 343 AA.
 AC 021669;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE R03G5.2 protein.
 GN R03G5.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
 OC Rhabdilitida; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; Pubmed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craction M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latelle P.,
RA Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Riffen L., Koopra A., Saunders D., Showkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Spratt J., Woldman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans".
RL Nature 368:32-38(1994).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL NZ;
RC Connell M.;
RA "The sequence of C. elegans cosmid R0365."
RT Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
RL [3]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL NZ;
RC Waterston R.;
RA Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL, U519194; AAA96067.1; "-"
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR ATP-binding, Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 343 AA; 39404 MW; 29237BB34226C12A CRC64;

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Query Match Similarity      50.0%; Score 865.5; DB 5; Length 343;
Best Local Similarity      50.8%; Pred. No. 2.5e-66;
Matches 168; Conservative 64; Mismatches 88; Indels 11; Gaps 6

QY      2   QSKGRKRN-PGLIKIDKEAFEPDQTSSTPRDLDSKACISIGNON--FEVKADDLPEIML 58
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      2   ERKGGRERKIPGKRI-----VMPETPVETPMNLDEKLLILTNSESEIEILAAIDLVLLEAL 56
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      59   GKGAGVYVEKKMHVPSGGOIMAVKRIATVNSOERKRLMDLDIIMRTVDCPFTVTEYGAL 118
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      57   GGGGIGVIEKMOHROSGLIMAVKRIKSSINDOSOKOMLNEIDACRSDDCPQWVRRTYGAM 116
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      119  FREGDWMICMELMDTSLDKFYKOVIDRGOTIPEIDILIGKLTAVSIKVALEHLHSKLSYIHD 178
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      117  FREGDWMICMEVMDTSLDFRYRHAYKIGIHIEPEFIFGKMAISIEGLNFMKBEOLNIHSD 176
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      179  VKPSNVNLALQVYKMCDFGISGLYVDSAKTIDACKCKRYMAPERINPELNOKGYSVSKD 238
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      177  VKPSNLLNRRHQVAKCDGFIGHLTNLSNAKTVOACIKKKKKKKKKKKKKKKKKKKKKKKKKKK 235
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      239  IWSLGTITMIEILAIRPYDSMGTPFEQOLQOVVEEESPOLPADK-FSAEEVDFTSQCLKN 297
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      236  VWSLGTITIEINVGTHPYANMKTPPEQLQOVVKEPPKLPMESGFVSDQYEVKRCLEKD 295
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      298  SKERPTYPELMOHPFF-TLHESKGDIVASV 327
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      296  YNERPKYPPELLAMPFEMEQARNEKQFSMARPI 326
      1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
Q9DGR7
ID      Q9DGR7      PRELIMINARY;      PRT;      281 AA.
AC      Q9DGR7;
DT      01-MAR-2001 (TEMBLrel. 16, Created)
DT      01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT      01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE      MKK4.
GN      ZMKR4.

```

OS Brachydanio rerio (zebrafish) (*Zebra danio*).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
CC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirano T., Fujii R., Hibi M.;
RT "Zebrafish MKK4.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB030901; BAB11811.1; -.
DR InterPro: IPR0000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase.1.
DR ProDom: PD000001; Euk_Pkinase.1.
DR SMART: SMO0220; S_Tkc.1.
DR SMART: SMO0219; TyrKc.1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 261 AA; 32304 MW; 438CFE0BDE1C1FA CRC64;

Query Match	49.1%	Score 850;	DB 153;	Length 281;
Best Local Similarity	59.2%	Pred. No. 4.1e-65;		
Matches 158;	Conservative 44;	Mismatches 61;	Indels 4;	Gaps 2;

QY	69	MHRPDSGIMAVKTRIRAYVNSQEQKRLMLDISMTVDCEPTVTFYGFALFREGDWTICM	128
DB	1	MAHKSQGIIMAVKTRIRSTYDEREQKQLMDLDVVRSSDCPIYVFGALFREGQWICM	60
QY	129	ELMDPSLRFKYFOVKD--GQTIPEDILKIAVSIYKALEHLHSLKSVIHRDVKPSNVLIN	187
DB	61	ELMSTSFQKFKYXYVSSLDEVPBEILIGITLTAVALNHLKEINKIITHRIDKPSNILLD	120
QY	188	ALGVKMKDFGISGLVNSVAKTTIDAGCGPYAPRINPELNQKGYSKSDIMSGITMI	247
DB	121	RKGNKIRLDFGISTGVLNDSIAKTRDQACRPYAPERIDPSASRGQIDVARSVMWSGITILY	180
QY	248	ELAIIRFPYDSNGTFPOOLKOYVEEBSPOLPAD--KESAEFVDFTSOCLKNSKSERPY	304
DB	181	ELATGRFPYPKNNSVFDOLTVQVKGDPOLSSSEEROFSPKINIFVNLCLTRDESKRPXY	240
QY	305	PFLMQHPEFTLHESKGTDVASFVKIL 331	
DB	241	KELLNHAFIQTMEKRSVDVAITYCRIL 267	

Search completed: June 6, 2003, 09:11:27
Job time : 35 secs